Method for distinguishing leukemia subtypes

The present invention is directed to a method for distinguishing leukemia subtypes, in particular leukemia subtypes AML with t(15;17), t(8;21), inv(16), inv(3), complex aberrant karyotype (CA), AML-MLL, normal karyotype (NK), AML-other, i.e. trisomy 8, trisomy 11, trisomy 13, monosomy 7, del(5q), del(9q), t(6;9); del(20q) and del(12p) and trisomy 4, ALL-MLL, ALL-Ph+, ALL-t(8;14), T-ALL, other B-lineage (OBL), CML, normal-BM (bone marrow), and/or CLL, by determining the expression level of selected marker genes.

Leukemias are classified into four different groups or types: acute myeloid (AML), acute lymphatic (ALL), chronic myeloid (CML) and chronic lymphatic leukemia (CLL). Within these groups, several subcategories can be identified further using a panel of standard techniques as described below. These different subcatgories in leukemias are associated with varying clinical outcome and therefore are the basis for different treatment strategies. The importance of highly specific classification may be illustrated in detail further for the AML as a very heterogeneous group of diseases. Effort is aimed at identifying biological entities and to distinguish and classify subgroups of AML which are associated with a favorable, intermediate or unfavorable prognosis, respectively. In 1976, the FAB classification was proposed by the French-American-British co-operative group which was based on cytomorphology and cytochemistry in order to separate AML subgroups according to the morphological appearance of blasts in the blood and bone marrow. In addition, it was recognized that genetic abnormalities occurring in the leukemic blast had a major impact on the morphological picture and even more on the prognosis. So far, the karyotype of the leukemic blasts is the most important independent prognostic factor regarding response to therapy as well as survival.

Usually, a combination of methods is necessary to obtain the most important information in leukemia diagnostics: Analysis of the morphology and cytochemistry of bone marrow blasts and peripheral blood cells is necessary to establish the diagnosis. In some cases the addition of immunophenotyping is mandatory to separate very undifferentiated AML from acute lymphoblastic leukemia and CLL. Leukemia subtypes investigated can be diagnosed by cytomorphology alone, only if an expert reviews the smears. However, a genetic

analysis based on chromosome analysis, fluorescence in situ hybridization or RT-PCR and immunophenotyping is required in order to assign all cases in to the right category. The aim of these techniques besides diagnosis is mainly to determine the prognosis of the leukemia. A major disadvantage of these methods, however, is that viable cells are necessary as the cells for genetic analysis have to divide in vitro in order to obtain metaphases for the analysis. Another problem is the long time of 72 hours from receipt of the material in the laboratory to obtain the result. Furthermore, great experience in preparation of chromosomes and even more in analyzing the karyotypes is required to obtain the correct result in at least 90% of cases. Using these techniques in combination, hematological malignancies in a first approach are separated into chronic myeloid leukemia (CML), chronic lymphoid (CLL), acute lymphoblastic (ALL), and acute myeloid leukemia (AML). Within the latter three disease entities several prognostically relevant subtypes have been established. As a second approach this further sub-classification is based mainly on genetic abnormalities of the leukemic blasts and clearly is associated with different prognoses.

The sub-classification of leukemias becomes increasingly important to guide therapy. The development of new, specific drugs and treatment approaches requires the identification of specific subtypes that may benefit from a distinct therapeutic protocol and, thus, can improve outcome of distinct subsets of leukemia. For example, the new therapeutic drug (STI571) inhibits the CML specific chimeric tyrosine kinase BCR-ABL generated from the genetic defect observed in CML, the BCR-ABL-rearrangement due to the translocation between chromosomes 9 and 22 (t(9;22) (q34; q11)). In patients treated with this new drug, the therapy response is dramatically higher as compared to all other drugs that had been used so far. Another example is the subtype of acute myeloid leukemia AML M3 and its variant M3v both with karyotype t(15;17)(q22; q11-12). The introduction of a new drug (all-trans retinoic acid - ATRA) has improved the outcome in this subgroup of patient from about 50% to 85 % long-term survivors. As it is mandatory for these patients suffering from these specific leukemia subtypes to be identified as fast as possible so that the best therapy can be applied, diagnostics today must accomplish sub-classification with maximal precision. Not only for these subtypes but also for several other leukemia subtypes different treatment approaches could improve outcome. Therefore, rapid and precise identification of distinct leukemia subtypes is the future goal for diagnostics.

Thus, the technical problem underlying the present invention was to provide means for leukemia diagnostics which overcome at least some of the disadvantages of the prior art diagnostic methods, in particular encompassing the time-consuming and unreliable combination of different methods and which provides a rapid assay to unambigously distinguish one AML subtype from another, e.g. by genetic analysis.

According to Golub et al. (Science, 1999, 286, 531-7), gene expression profiles can be used for class prediction and discriminating AML from ALL samples. However, for the analysis of acute leukemias the selection of the two different subgroups was performed using exclusively morphologic-phenotypical criteria. This was only descriptive and does not provide deeper insights into the pathogenesis or the underlying biology of the leukemia. The approach reproduces only very basic knowledge of cytomorphology and intends to differentiate classes. The data is not sufficient to predict prognostically relevant cytogenetic aberrations.

Furthermore, the international application WO-A 03/039443 discloses marker genes the expression levels of which are characteristic for certain leukemia, e.g. AML subtypes and additionally discloses methods for differentiating between the subtype of AML cells by determining the expression profile of the disclosed marker genes. However, WO-A 03/039443 does not provide guidance which set of distinct genes discriminate between two subtypes and, as such, can be routineously taken in order to distinguish one leukemia subtype from another.

The problem is solved by the present invention, which provides a method for distinguishing leukemia subtypes t(15;17), t(8;21), inv(16), inv(3), complex aberrant karyotype (CA), AML-MLL, normal karyotype (NK), AML-other (trisomy 8, trisomy 11, trisomy 13, monosomy 7, del(5q), del(9q), t(6;9); del(20q) and del(12p) and trisomy 4), ALL-MLL, ALL-Ph+, ALL-t(8;14), T-ALL, other B-lineage (OBL), CML, normal-BM, and/or CLL in a sample, the method comprising determining the expression level of markers selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1 and/or 2,

wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.1 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.1 having a positive fc value,

is indicative for the presence ALL_MLL when ALL_MLL is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.2 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.2 having a positive fc value,

is indicative for the presence ALL_Ph+ when ALL_Ph+ is distinguished from all other subtypes;

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.3 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.3 having a positive fc value,

is indicative for the presence ALL_T lineage when ALL_T lineage is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.4 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.4 having a positive fc value,

is indicative for the presence ALL_t(8;14) when ALL_t(8;14) is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.5 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.5 having a positive fc value,

is indicative for the presence AML_MLL when AML_MLL is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.6 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.6 having a positive fc value,

is indicative for the presence AML_inv(16) when AML_inv(16) is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.7 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.7 having a positive fc value,

is indicative for the presence AML_inv(3) when AML_inv(3) is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.8 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.8 having a positive fc value,

is indicative for the presence AML_komplext when AML_komplext is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.9 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.9 having a positive fc value,

is indicative for the presence AML_t(15;17) when AML_t(15;17) is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.10 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.10 having a positive fc value,

is indicative for the presence AML_t(8;21) when AML_t(8;21) is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.11 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.11 having a positive fc value,

is indicative for the presence CLL when CLL is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.12 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.12 having a positive fc value,

is indicative for the presence CML when CML is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.13 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 1.13 having a positive fc value,

is indicative for the presence normal-BM when normal-BM is distinguished from all leukemia subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.1 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.1 having a positive fc value,

is indicative for the presence ALL_MLL when ALL_MLL is distinguished from ALL_Ph+,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.2 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.2 having a positive fc value,

is indicative for the presence ALL_MLL when ALL_MLL is distinguished from ALL_T lineage,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.3 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.3 having a positive fc value,

is indicative for the presence ALL_MLL when ALL_MLL is distinguished from ALL_t(8;14),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.4 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.4 having a positive fc value,

is indicative for the presence ALL_MLL when ALL_MLL is distinguished from AML_MLL,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.5 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.5 having a positive fc value,

is indicative for the presence ALL_MLL when ALL_MLL is distinguished from AML_inv(16),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.6 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.6 having a positive fc value,

is indicative for the presence ALL_MLL when ALL_MLL is distinguished from AML_inv(3),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.7 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.7 having a positive fc value,

is indicative for the presence ALL_MLL when ALL_MLL is distinguished from AML_komplext,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.8 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.8 having a positive fc value,

is indicative for the presence ALL_MLL when ALL_MLL is distinguished from AML_t(15;17),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.9 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.9 having a positive fc value,

is indicative for the presence ALL_MLL when ALL_MLL is distinguished from AML_t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.10 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.10 having a positive fc value,

is indicative for the presence ALL_MLL when ALL_MLL is distinguished from CLL,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.11 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.11 having a positive fc value,

is indicative for the presence ALL_MLL when ALL_MLL is distinguished from CML,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.12 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.12 having a positive fc value,

is indicative for the presence ALL_MLL when ALL_MLL is distinguished from normal-BM,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.13 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.13 having a positive fc value,

is indicative for the presence ALL_Ph+ when ALL_Ph+ is distinguished from ALL_T lineage,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.14 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.14 having a positive fc value,

is indicative for the presence ALL_Ph+ when ALL_Ph+ is distinguished from ALL_t(8;14),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.15 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.15 having a positive fc value,

is indicative for the presence ALL_Ph+ when ALL_Ph+ is distinguished from AML_MLL,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.16 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.16 having a positive fc value,

is indicative for the presence ALL_Ph+ when ALL_Ph+ is distinguished from AML_inv(16),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.17 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.17 having a positive fc value,

is indicative for the presence ALL_Ph+ when ALL_Ph+ is distinguished from AML_inv(3),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.18 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.18 having a positive fc value,

is indicative for the presence ALL_Ph+ when ALL_Ph+ is distinguished from AML_komplext,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.19 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.19 having a positive fc value,

is indicative for the presence ALL_Ph+ when ALL_Ph+ is distinguished from AML_t(15;17),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.20 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.20 having a positive fc value,

is indicative for the presence ALL_Ph+ when ALL_Ph+ is distinguished from AML_t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.21 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.21 having a positive fc value,

is indicative for the presence ALL_Ph+ when ALL_Ph+ is distinguished from CLL,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.22 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.22 having a positive fc value,

is indicative for the presence ALL_Ph+ when ALL_Ph+ is distinguished from CML,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.23 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.23 having a positive fc value,

is indicative for the presence ALL_Ph+ when ALL_Ph+ is distinguished from normal-BM,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.24 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.24 having a positive fc value,

is indicative for the presence ALL_T lineage when ALL_T lineage distinguished from ALL_t(8;14),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.25 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.25 having a positive fc value,

is indicative for the presence ALL_T lineage when ALL_T lineage distinguished from AML_MLL,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.26 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.26 having a positive fc value,

is indicative for the presence ALL_T lineage when ALL_T lineage distinguished from AML_inv(16),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.27 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.27 having a positive fc value,

is indicative for the presence ALL_T lineage when ALL_T lineage distinguished from AML_inv(3),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.28 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.28 having a positive fc value,

is indicative for the presence ALL_T lineage when ALL_T lineage distinguished from AML_komplext,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.29 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.29 having a positive fc value,

is indicative for the presence ALL_T lineage when ALL_T lineage distinguished from AML_t(15;17),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.30 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.30 having a positive fc value,

is indicative for the presence ALL_T lineage when ALL_T lineage distinguished from AML_t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.31 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.31 having a positive fc value,

is indicative for the presence ALL_T lineage when ALL_T lineage distinguished from CLL,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.32 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.32 having a positive fc value,

is indicative for the presence ALL_T lineage when ALL_T lineage distinguished from CML,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.33 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.33 having a positive fc value,

is indicative for the presence ALL_T lineage when ALL_T lineage distinguished from normal-BM,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.34 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.34 having a positive fc value,

is indicative for the presence ALL_t(8;14) when ALL_t(8;14) distinguished from AML_MLL,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.35 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.35 having a positive fc value,

is indicative for the presence ALL_t(8;14) when ALL_t(8;14) distinguished from AML_inv(16),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.36 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.36 having a positive fc value,

is indicative for the presence ALL_t(8;14) when ALL_t(8;14) distinguished from AML_inv(3),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.37 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.37 having a positive fc value,

is indicative for the presence ALL_t(8;14) when ALL_t(8;14) distinguished from AML_komplext,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.38 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.38 having a positive fc value,

is indicative for the presence ALL_t(8;14) when ALL_t(8;14) distinguished from AML_t(15;17),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.39 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.39 having a positive fc value,

is indicative for the presence ALL_t(8;14) when ALL_t(8;14) distinguished from AML_t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.40 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.40 having a positive fc value,

is indicative for the presence ALL_t(8;14) when ALL_t(8;14) distinguished from CLL,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.41 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.41 having a positive fc value,

is indicative for the presence ALL_t(8;14) when ALL_t(8;14) distinguished from CML,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.42 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.42 having a positive fc value,

is indicative for the presence ALL_t(8;14) when ALL_t(8;14) distinguished from normal-BM,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.43 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.43 having a positive fc value,

is indicative for the presence AML_MLL when AML_MLL distinguished from AML_inv(16),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.44 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.44 having a positive fc value,

is indicative for the presence AML_MLL when AML_MLL distinguished from AML_inv(3),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.45 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.45 having a positive fc value,

is indicative for the presence AML_MLL when AML_MLL distinguished from AML_komplext,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.46 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.46 having a positive fc value,

is indicative for the presence AML_MLL when AML_MLL distinguished from AML_t(15;17),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.47 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.47 having a positive fc value,

is indicative for the presence AML_MLL when AML_MLL distinguished from AML_t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.48 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.48 having a positive fc value,

is indicative for the presence AML_MLL when AML_MLL distinguished from CLL,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.49 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.49 having a positive fc value,

is indicative for the presence AML_MLL when AML_MLL distinguished from CML,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.50 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.50 having a positive fc value,

is indicative for the presence AML_MLL when AML_MLL distinguished from normal-BM,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.51 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.51 having a positive fc value,

is indicative for the presence AML_inv(16) when AML_inv(16) distinguished from AML_inv(3),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.52 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.52 having a positive fc value,

is indicative for the presence AML_inv(16) when AML_inv(16) distinguished from AML_komplext,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.53 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.53 having a positive fc value,

is indicative for the presence AML_inv(16) when AML_inv(16) distinguished from AML_t(15;17),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.54 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.54 having a positive fc value,

is indicative for the presence AML_inv(16) when AML_inv(16) distinguished from AML_t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.55 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.55 having a positive fc value,

is indicative for the presence AML_inv(16) when AML_inv(16) distinguished from CLL,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.56 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.56 having a positive fc value,

is indicative for the presence AML_inv(16) when AML_inv(16) distinguished from CML,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.57 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.57 having a positive fc value,

is indicative for the presence AML_inv(16) when AML_inv(16) distinguished from normal-BM,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.58 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.58 having a positive fc value,

is indicative for the presence AML_inv(3) when AML_inv(3) distinguished from AML_komplext,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.59 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.59 having a positive fc value,

is indicative for the presence AML_inv(3) when AML_inv(3) distinguished from AML_t(15;17),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.60 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.60 having a positive fc value,

is indicative for the presence AML_inv(3) when AML_inv(3) distinguished from AML_t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.61 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.61 having a positive fc value,

is indicative for the presence AML_inv(3) when AML_inv(3) distinguished from CLL,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.62 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.62 having a positive fc value,

is indicative for the presence AML_inv(3) when AML_inv(3) distinguished from CML,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.63 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.63 having a positive fc value,

is indicative for the presence AML_inv(3) when AML_inv(3) distinguished from normal-BM,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.64 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.64 having a positive fc value,

is indicative for the presence AML_komplext when AML_komplext distinguished from AML_t(15;17),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.65 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.65 having a positive fc value,

is indicative for the presence AML_komplext when AML_komplext distinguished from AML_t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.66 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.66 having a positive fc value,

is indicative for the presence AML_komplext when AML_komplext distinguished from CLL,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.67 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.67 having a positive fc value,

is indicative for the presence AML_komplext when AML_komplext distinguished from CML,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.68 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.68 having a positive fc value,

is indicative for the presence AML_komplext when AML_komplext distinguished from normal-BM,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.69 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.69 having a positive fc value,

is indicative for the presence AML_t(15;17) when AML_t(15;17) is distinguished from AML_t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.70 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.70 having a positive fc value,

is indicative for the presence AML_t(15;17) when AML_t(15;17) is distinguished from CLL,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.71 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.71 having a positive fc value,

is indicative for the presence AML_t(15;17) when AML_t(15;17) is distinguished from CML,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.72 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.72 having a positive fc value,

is indicative for the presence AML_t(15;17) when AML_t(15;17) is distinguished from normal-BM,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.73 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.73 having a positive fc value,

is indicative for the presence AML_t(8;21) when AML_t(8;21) is distinguished from CLL,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.74 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.74 having a positive fc value,

is indicative for the presence AML_t(8;21) when AML_t(8;21) is distinguished from CML,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.75 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.75 having a positive fc value,

is indicative for the presence AML_t(8;21) when AML_t(8;21) is distinguished from normal-BM,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.76 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.76 having a positive fc value,

is indicative for the presence CLL when CLL is distinguished from CML,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.77 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.77 having a positive fc value,

is indicative for the presence CLL when CLL is distinguished from normal-BM,

and/or wherein

a lower expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.78 having a negative fc value, and/or

a higher expression of at least one polynucleotide defined by at least one of the numbers 1 to 50 of Table 2.78 having a positive fc value,

is indicative for the presence CML when CML is distinguished from normal-BM.

As used herein, the following definitions apply to the above abbreviations:

t(15;17): AML with t(15;17) translocation

t(8;21): AML with t(8;21) translocation

inv(16): AML with inversion 16

inv(3): AML with inversion 3

CA: AML with complex aberrant karyotype

AML-MLL: AML with mutations on the mixed lineage leukaemia (MLL) gene

normal karyotype (NK): AML with normal karyotype

trisomy 8: AML with trisomy of chromosome 8

trisomy 11: AML with trisomy of chromosome 11

trisomy 13:AML with trisomy of chromosome 13

monosomy 7: AML with monosomy of chromosome 7

del(5q): AML with 5q deletion

del(9q): AML with 9q deletion

t(6;9): AML with t(6;9) translocation

del(20q): AML with 20 q deletion

del(12p): AML with deletion 12 p deletion

trisomy 4: AML with trisomy 4

ALL-MLL: acute lymphoblastic leukaemia with mutations on the mixed lineage leukemia (MLL) gene

ALL-Ph+: acute lymphoblastic leukaemia with genetic aberration on the Philadelphia chromosome

ALL-t(8;14): acute lymphoblastic leukemia with translocation t(8;21)

T-ALL: T cell acute lymphoblastic leukemia

other B-lineage (OBL):

CML: chronic myeloid leukemia

normal-BM: bone marrow from healthy volunteers

CLL: chronic lymphatic leukemia

As used herein, "all other subtypes" refer to the subtypes of the present invention, i.e. to all other subtypes except for the one being under investigation

According to the present invention, a "sample" means any biological material containing genetic information in the form of nucleic acids or proteins obtainable or obtained from an individual. The sample includes e.g. tissue samples, cell samples, bone marrow and/or body fluids such as blood, saliva, semen. Preferably, the sample is blood or bone marrow, more preferably the sample is bone marrow. The person skilled in the art is aware of methods, how to isolate nucleic acids and proteins from a sample. A general method for isolating and preparing nucleic acids from a sample is outlined in Example 3.

According to the present invention, the term "lower expression" is generally assigned to all by numbers and Affymetrix Id. definable polynucleotides the t-values and fold change (fc) values of which are negative, as indicated in the Tables. Accordingly, the term "higher expression" is generally assigned to all by numbers and Affymetrix Id. definable polynucleotides the t-values and fold change (fc) values of which are positive.

According to the present invention, the term "expression" refers to the process by which mRNA or a polypeptide is produced based on the nucleic acid sequence of a gene, i.e. „expression" also includes the formation of mRNA upon transcription. In accordance with the present invention, the term „determining the expression level" preferably refers to the determination of the level of expression, namely of the markers.

Generally, "marker" refers to any genetically controlled difference which can be used in the genetic analysis of a test versus a control sample, for the purpose of assigning the sample to a defined genotype or phenotype. As used herein, "markers" refer to genes which are differentially expressed in, e.g., different AML subtypes. The markers can be defined by their gene symbol name, their encoded protein name, their transcript identification number (cluster identification number), the data base accession number, public accession number or GenBank identifier or,

as done in the present invention, Affymetrix identification number, chromosomal location, UniGene accession number and cluster type, LocusLink accession number (see Examples and Tables).

The Affymetrix identification number (affy id) is accessible for anyone and the person skilled in the art by entering the "gene expression omnibus" internet page of the National Center for Biotechnology Information (NCBI) (http://www.ncbi.nlm.nih.gov/geo/). In particular, the affy id's of the polynucleotides used for the method of the present invention are derived from the so-called U133 chip. The sequence data of each identification number can be viewed at http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL96

Generally, the expression level of a marker is determined by the determining the expression of its corresponding "polynucleotide" as described hereinafter.

According to the present invention, the term „polynucleotide" refers, generally, to a DNA, in particular cDNA, or RNA, in particular a cRNA, or a portion thereof or a polypeptide or a portion thereof. In the case of RNA (or cDNA), the polynucleotide is formed upon transcription of a nucleotide sequence which is capable of expression. The polynucleotide fragments refer to fragments preferably of between at least 8, such as 10, 12, 15 or 18 nucleotides and at least 50, such as 60, 80, 100, 200 or 300 nucleotides in length, or a complementary sequence thereto, representing a consecutive stretch of nucleotides of a gene, cDNA or mRNA. In other terms, polynucleotides include also any fragment (or complementary sequence thereto) of a sequence derived from any of the markers defined above as long as these fragments unambiguously identify the marker.

The determination of the expression level may be effected at the transcriptional or translational level, i.e. at the level of mRNA or at the protein level. Protein fragments such as peptides or polypeptides advantageously comprise between at least 6 and at least 25, such as 30, 40, 80, 100 or 200 consecutive amino acids representative of the corresponding full length protein. Six amino acids are generally recognized as the lowest peptidic stretch giving rise to a linear epitope recognized by an antibody, fragment or derivative thereof. Alternatively, the

proteins or fragments thereof may be analysed using nucleic acid molecules specifically binding to three-dimensional structures (aptamers).

Depending on the nature of the polynucleotide or polypeptide, the determination of the expression levels may be effected by a variety of methods. For determining and detecting the expression level, it is preferred in the present invention that the polynucleotide, in particular the cRNA, is labelled.

The labelling of the polynucleotide or a polypeptide can occur by a variety of methods known to the skilled artisan. The label can be fluorescent, chemiluminescent, bioluminescent, radioactive (such as ^{3}H or ^{32}P). The labelling compound can be any labelling compound being suitable for the labelling of polynucleotides and/or polypeptides. Examples include fluorescent dyes, such as fluorescein, dichlorofluorescein, hexachlorofluorescein, BODIPY variants, ROX, tetramethylrhodamin, rhodamin X, Cyanine-2, Cyanine-3, Cyanine-5, Cyanine-7, IRD40, FluorX, Oregon Green, Alexa variants (available e.g. from Molecular Probes or Amersham Biosciences) and the like, biotin or biotinylated nucleotides, digoxigenin, radioisotopes, antibodies, enzymes and receptors. Depending on the type of labelling, the detection is done via fluorescence measurements, conjugation to streptavidin and/or avidin, antigen-antibody- and/or antibody-antibody-interactions, radioactivity measurements, as well as catalytic and/or receptor/ligand interactions. Suitable methods include the direct labelling (incorporation) method, the amino-modified (amino-allyl) nucleotide method (available e.g. from Ambion), and the primer tagging method (DNA dendrimer labelling, as kit available e.g. from Genisphere). Particularly preferred for the present invention is the use of biotin or biotinylated nucleotides for labelling, with the latter being directly incorporated into, e.g. the cRNA polynucleotide by in vitro transcription.

If the polynucleotide is mRNA, cDNA may be prepared into which a detectable label, as exemplified above, is incorporated. Said detectably labelled cDNA, in single-stranded form, may then be hybridised, preferably under stringent or highly stringent conditions to a panel of single-stranded oligonucleotides representing different genes and affixed to a solid support such as a chip. Upon applying appropriate washing steps, those cDNAs will be detected or quantitatively detected that have a counterpart in the oligonucleotide panel. Various advantageous embodiments of this general method are feasible. For example, the mRNA or the

cDNA may be amplified e.g. by polymerase chain reaction, wherein it is preferable, for quantitative assessments, that the number of amplified copies corresponds relative to further amplified mRNAs or cDNAs to the number of mRNAs originally present in the cell. In a preferred embodiment of the present in ivention, the cDNAs are transcribed into cRNAs prior to the hybridisation step wherein only in the transcription step a label is incorporated into the nucleic acid and wherein the cRNA is employed for hybridisation. Alternatively, the label may be attached subsequent to the transcription step.

Similarly, proteins from a cell or tissue under investigation may be contacted with a panel of aptamers or of antibodies or fragments or derivatives thereof. The antibodies etc. may be affixed to a solid support such as a chip. Binding of proteins indicative of an AML subtype may be verified by binding to a detectably labelled secondary antibody or aptamer. For the labelling of antibodies, it is referred to Harlow and Lane, "Antibodies, a laboratory manual", CSH Press, 1988, Cold Spring Harbor. Specifically, a minimum set of proteins necessary for diagnosis of all leukemia subtypes may be selected for creation of a protein array system to make diagnosis on a protein lysate of a diagnostic bone marrow sample directly. Protein Array Systems for the detection of specific protein expression profiles already are available (for example: Bio-Plex, BIORAD, München, Germany). For this application preferably antibodies against the proteins have to be produced and immobilized on a platform e.g. glasslides or microtiterplates. The immobilized antibodies can be labelled with a reactant specific for the certain target proteins as discussed above. The reactants can include enzyme substrates, DNA, receptors, antigens or antibodies to create for example a capture sandwich immunoassay.

For reliably distinguishing Leukemia subtypes t(15;17), t(8;21), inv(16), inv(3), complex aberrant karyotype (CA), AML-MLL, normal karyotype (NK), AML-other, i.e. trisomy 8, trisomy 11, trisomy 13, monosomy 7, del(5q), del(9q), t(6;9); del(20q) and del(12p) and trisomy 4, ALL-MLL, ALL-Ph+, ALL-t(8;14), T-ALL, other B-lineage (OBL), CML, normal-BM, and/or CLL it is useful that the expression of more than one of the above defined markers. As a criterion for the choice of markers, the statistical significance of markers as expressed in q or p values based on the concept of the false discovery rate is determined. In doing so, a measure of statistical significance called the *q* value is associated with each tested

feature. The *q* value is similar to the *p* value, except it is a measure of significance in terms of the false discovery rate rather than the false positive rate (Storey JD and Tibshirani R. Proc.Natl.Acad.Sci., 2003, Vol. 100:9440-5.

In a preferred embodiment of the present invention, markers as defined in Tables 1.1-2.78 having a q-value of less than 3E-06, more preferred less than 1.5E-09, most preferred less than 1.5E-11, less than 1.5E-20, less than 1.5E-30, are measured.

Of the above defined markers, the expression level of at least two, preferably of at least ten, more preferably of at least 25, most preferably of 50 of at least one of the Tables of the markers is determined.

In another preferred embodiment, the expression level of at least 2, of at least 5, of at least 10 out of the markers having the numbers 1 – 10, 1-20, 1-40, 1-50 of at least one of the Tables are measured.

The level of the expression of the „marker", i.e. the expression of the polynucleotide is indicative of the leukemia subtype of a cell or an organism. The level of expression of a marker or group of markers is measured and is compared with the level of expression of the same marker or the same group of markers from other cells or samples. The comparison may be effected in an actual experiment or in silico. When the expression level also referred to as expression pattern or expression signature (expression profile) is measurably different, there is according to the invention a meaningful difference in the level of expression. Preferably the difference at least is 5 %, 10% or 20%, more preferred at least 50% or may even be as high as 75% or 100%. More preferred the difference in the level of expression is at least 200%, i.e. two fold, at least 500%, i.e. five fold, or at least 1000%, i.e. 10 fold.

Accordingly, the expression level of markers expressed lower in a first subtype than in at least one second subtype, which differs from the first subtype, is at least 5 %, 10% or 20%, more preferred at least 50% or may even be 75% or 100%, i.e. 2-fold lower, preferably at least 10-fold, more preferably at least 50-fold, and most preferably at least 100-fold lower in the first subtype. On the other hand, the expression level of markers expressed higher in a first subtype than in at least one

second subtype, which differs from the first subtype, is at least 5 %, 10% or 20%, more preferred at least 50% or may even be 75% or 100%, i.e. 2-fold higher, preferably at least 10-fold, more preferably at least 50-fold, and most preferably at least 100-fold higher in the first subtype.

In another embodiment of the present invention, the sample is derived from an individual having leukemia.

For the method of the present invention it is preferred if the polynucleotide the expression level of which is determined is in form of a transcribed polynucleotide. A particularly preferred transcribed polynucleotide is an mRNA, a cDNA and/or a cRNA, with the latter being preferred. Transcribed polynucleotides are isolated from a sample, reverse transcribed and/or amplified, and labelled, by employing methods well-known the person skilled in the art (see Example 3). In a preferred embodiment of the methods according to the invention, the step of determining the expression profile further comprises amplifying the transcribed polynucleotide.

In order to determine the expression level of the transcribed polynucleotide by the method of the present invention, it is preferred that the method comprises hybridizing the transcribed polynucleotide to a complementary polynucleotide, or a portion thereof, under stringent hybridization conditions, as described hereinafter.

The term "hybridizing" means hybridization under conventional hybridization conditions, preferably under stringent conditions as described, for example, in Sambrook, J., et al., in "Molecular Cloning: A Laboratory Manual" (1989), Eds. J. Sambrook, E. F. Fritsch and T. Maniatis, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, NY and the further definitions provided above. Such conditions are, for example, hybridization in 6x SSC, pH 7.0 / 0.1% SDS at about 45°C for 18-23 hours, followed by a washing step with 2x SSC/0.1% SDS at 50°C. In order to select the stringency, the salt concentration in the washing step can for example be chosen between 2x SSC/0.1% SDS at room temperature for low stringency and 0.2x SSC/0.1% SDS at 50°C for high stringency. In addition, the temperature of the washing step can be varied between room temperature, ca. 22°C, for low stringency, and 65°C to 70° C for high stringency. Also contemplated are polynucleotides that hybridize at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily

accomplished through the manipulation, preferably of formamide concentration (lower percentages of formamide result in lowered stringency), salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH2PO4; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 mg/ml salmon sperm blocking DNA, followed by washes at 50°C with 1 X SSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5x SSC). Variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

"Complementary" and "complementarity", respectively, can be described by the percentage, i.e. proportion, of nucleotides which can form base pairs between two polynucleotide strands or within a specific region or domain of the two strands. Generally, complementary nucleotides are, according to the base pairing rules, adenine and thymine (or adenine and uracil), and cytosine and guanine. Complementarity may be partial, in which only some of the nucleic acids' bases are matched according to the base pairing rules. Or, there may be a complete or total complementarity between the nucleic acids. The degree of complementarity between nucleic acid strands has effects on the efficiency and strength of hybridization between nucleic acid strands.

Two nucleic acid strands are considered to be 100% complementary to each other over a defined length if in a defined region all adenines of a first strand can pair with a thymine (or an uracil) of a second strand, all guanines of a first strand can pair with a cytosine of a second strand, all thymine (or uracils) of a first strand can pair with an adenine of a second strand, and all cytosines of a first strand can pair with a guanine of a second strand, and vice versa. According to the present invention, the degree of complementarity is determined over a stretch of 20, preferably 25, nucleotides, i.e. a 60% complementarity means that within a region of 20 nucleotides of two nucleic acid strands 12 nucleotides of the first strand can base pair with 12 nucleotides of the second strand according to the above ruling, either as a stretch of 12 contiguous nucleotides or interspersed by non-pairing nucleotides, when the two strands are attached to each other over said region of 20

nucleotides. The degree of complementarity can range from at least about 50% to full, i.e. 100% complementarity. Two single nucleic acid strands are said to be "substantially complementary" when they are at least about 80% complementary, preferably about 90% or higher. For carrying out the method of the present invention substantial complementarity is preferred.

Preferred methods for detection and quantification of the amount of polynucleotides, i.e. for the methods according to the invention allowing the determination of the level of expression of a marker, are those described by Sambrook et al. (1989) or real time methods known in the art as the TaqMan® method disclosed in WO92/02638 and the corresponding U.S. 5,210,015, U.S. 5,804,375, U.S. 5,487,972. This method exploits the exonuclease activity of a polymerase to generate a signal. In detail, the (at least one) target nucleic acid component is detected by a process comprising contacting the sample with an oligonucleotide containing a sequence complementary to a region of the target nucleic acid component and a labeled oligonucleotide containing a sequence complementary to a second region of the same target nucleic acid component sequence strand, but not including the nucleic acid sequence defined by the first oligonucleotide, to create a mixture of duplexes during hybridization conditions, wherein the duplexes comprise the target nucleic acid annealed to the first oligonucleotide and to the labeled oligonucleotide such that the 3'-end of the first oligonucleotide is adjacent to the 5'-end of the labeled oligonucleotide. Then this mixture is treated with a template-dependent nucleic acid polymerase having a 5' to 3' nuclease activity under conditions sufficient to permit the 5' to 3' nuclease activity of the polymerase to cleave the annealed, labeled oligonucleotide and release labeled fragments. The signal generated by the hydrolysis of the labeled oligonucleotide is detected and/ or measured. TaqMan® technology eliminates the need for a solid phase bound reaction complex to be formed and made detectable. Other methods include e.g. fluorescence resoance energy transfer between two adjacenly hybridized probes as used in the LightCycler® format described in U.S. 6,174,670.

A preferred protocol if the marker, i.e. the polynucleotide, is in form of a transcribed nucleotide, is described in Example 3, where total RNA is isolated, cDNA and, subsequently, cRNA is synthesized and biotin is incorporated during the transcription reaction. The purified cRNA is applied to commercially available

arrays which can be obtained e.g. from Affymetrix. The hybridized cRNA is detected according to the methods described in Example 3. The arrays are produced by photolithography or other methods known to experts skilled in the art e.g. from U.S. 5,445,934, U.S. 5,744,305, U.S. 5,700,637, U.S. 5,945,334 and EP 0 619 321 or EP 0 373 203, or as decribed hereinafter in greater detail.

In another embodiment of the present invention, the polynucleotide or at least one of the polynucleotides is in form of a polypeptide. In another preferred embodiment, the expression level of the polynucleotides or polypeptides is detected using a compound which specifically binds to the polynucleotide of the polypeptide of the present invention.

As used herein, "specifically binding" means that the compound is capable of discriminating between two or more polynucleotides or polypeptides, i.e. it binds to the desired polynucleotide or polypeptide, but essentially does not bind unspecifically to a different polynucleotide or polypeptide.

The compound can be an antibody, or a fragment thereof, an enzyme, a so-called small molecule compound, a protein-scaffold, preferably an anticalin. In a preferred embodiment, the compound specifically binding to the polynucleotide or polypeptide is an antibody, or a fragment thereof.

As used herein, an "antibody" comprises monoclonal antibodies as first described by Köhler and Milstein in Nature 278 (1975), 495-497 as well as polyclonal antibodies, i.e. entibodies contained in a polyclonal antiserum. Monoclonal antibodies include those produced by transgenic mice. Fragments of antibodies include $F(ab')_2$, Fab and Fv fragments. Derivatives of antibodies include scFvs, chimeric and humanized antibodies. See, for example Harlow and Lane, loc. cit. For the detection of polypeptides using antibodies or fragments thereof, the person skilled in the art is aware of a variety of methods, all of which are included in the present invention. Examples include immunoprecipitation, Western blotting, Enzyme-linked immuno sorbent assay (ELISA), Enzyme-linked immuno sorbent assay (RIA), dissociation-enhanced lanthanide fluoro immuno assay (DELFIA), scintillation proximity assay (SPA). For detection, it is desirable if the antibody is labelled by one of the labelling compounds and methods described supra.

In another preferred embodiment of the present invention, the method for distinguishing leukemia subtypes is carried out on an array.

In general, an "array" or "microarray" refers to a linear or two- or three dimensional arrangement of preferably discrete nucleic acid or polypeptide probes which comprises an intentionally created collection of nucleic acid or polypeptide probes of any length spotted onto a substrate/solid support. The person skilled in the art knows a collection of nucleic acids or polypeptide spotted onto a substrate/solid support also under the term "array". As known to the person skilled in the art, a microarray usually refers to a miniaturised array arrangement, with the probes being attached to a density of at least about 10, 20, 50, 100 nucleic acid molecules referring to different or the same genes per cm^2. Furthermore, where appropriate an array can be referred to as "gene chip". The array itself can have different formats, e.g. libraries of soluble probes or libraries of probes tethered to resin beads, silica chips, or other solid supports.

The process of array fabrication is well-known to the person skilled in the art. In the following, the process for preparing a nucleic acid array is described. Commonly, the process comprises preparing a glass (or other) slide (e.g. chemical treatment of the glass to enhance binding of the nucleic acid probes to the glass surface), obtaining DNA sequences representing genes of a genome of interest, and spotting sequences these sequences of interest onto glass slide. Sequences of interest can be obtained via creating a cDNA library from an mRNA source or by using publicly available databases, such as GeneBank, to annotate the sequence information of custom cDNA libraries or to identify cDNA clones from previously prepared libraries. Generally, it is recommendable to amplify obtained sequences by PCR in order to have sufficient amounts of DNA to print on the array. The liquid containing the amplified probes can be deposited on the array by using a set of microspotting pins. Ideally, the amount deposited should be uniform. The process can further include UV-crosslinking in order to enhance immobilization of the probes on the array.

In a preferred embodiment, the array is a high density oligonucleotide (oligo) array using a light-directed chemical synthesis process, employing the so-called photolithography technology. Unlike common cDNA arrays, oligo arrays (according to the Affymetrix technology) use a single-dye technology. Given the

sequence information of the markers, the sequence can be synthesized directly onto the array, thus, bypassing the need for physical intermediates, such as PCR products, required for making cDNA arrays. For this purpose, the marker, or partial sequences thereof, can be represented by 14 to 20 features, preferably by less than 14 features, more preferably less than 10 features, even more preferably by 6 features or less, with each feature being a short sequence of nucleotides (oligonucleotide), which is a perfect match (PM) to a segment of the respective gene. The PM oligonucleotide are paired with mismatch (MM) oligonucleotides which have a single mismatch at the central base of the nucleotide and are used as "controls". The chip exposure sites are defined by masks and are deprotected by the use of light, followed by a chemical coupling step resulting in the synthesis of one nucleotide. The masking, light deprotection, and coupling process can then be repeated to synthesize the next nucleotide, until the nucleotide chain is of the specified length.

Advantageously, the method of the present invention is carried out in a robotics system including robotic plating and a robotic liquid transfer system, e.g. using microfluidics, i.e. channelled structured.

A particular preferred method according to the present invention is as follows:

1. Obtaining a sample, e.g. bone marrow or peripheral blood aliquots, from a patient having leukemia
2. Extracting RNA, preferably mRNA, from the sample
3. Reverse transcribing the RNA into cDNA
4. In vitro transcribing the cDNA into cRNA
5. Fragmenting the cRNA
6. Hybridizing the fragmented cRNA on standard microarrays
7. Determining hybridization

In another embodiment, the present invention is directed to the use of at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, and/or 2 for the manufacturing of a diagnostic for distinguishing Leukemia subtypes. The use of the present invention is particularly advantageous for distinguishing leukemia subtypes in an individual having leukemia. The use of said markers for diagnosis of leukemia subtypes, preferably based on microarray technology, offers the following advantages: (1) more rapid and more precise diagnosis, (2) easy to use in laboratories without

specialized experience, (3) abolishes the requirement for analyzing viable cells for chromosome analysis (transport problem), and (4) very experienced hematologists for cytomorphology and cytochemistry, immunophenotyping as well as cytogeneticists and molecularbiologists are no longer required.

Accordingly, the present invention refers to a diagnostic kit containing at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, and/or 2 for distinguishing leukemia subtypes, in combination with suitable auxiliaries. Suitable auxiliaries, as used herein, include buffers, enzymes, labelling compounds, and the like. In a preferred embodiment, the marker contained in the kit is a nucleic acid molecule which is capable of hybridizing to the mRNA corresponding to at least one marker of the present invention. Preferably, the at least one nucleic acid molecule is attached to a solid support, e.g. a polystyrene microtiter dish, nitrocellulose membrane, glass surface or to non-immobilized particles in solution.

In another preferred embodiment, the diagnostic kit contains at least one reference for a t(15;17), t(8;21), inv(16), inv(3), complex aberrant karyotype (CA), AML-MLL, normal karyotype (NK), AML-other, i.e. trisomy 8, trisomy 11, trisomy 13, monosomy 7, del(5q), del(9q), t(6;9); del(20q) and del(12p) and trisomy 4, ALL-MLL, ALL-Ph+, ALL-t(8;14), T-ALL, other B-lineage (OBL), CML, normal-BM, and/or CLL leukemia subtype. As used herein, the reference can be a sample or a data bank.

In another embodiment, the present invention is directed to an apparatus for distinguishing leukemia subtypes t(15;17), t(8;21), inv(16), inv(3), complex aberrant karyotype (CA), AML-MLL, normal karyotype (NK), AML-other, i.e. trisomy 8, trisomy 11, trisomy 13, monosomy 7, del(5q), del(9q), t(6;9); del(20q) and del(12p) and trisomy 4, ALL-MLL, ALL-Ph+, ALL-t(8;14), T-ALL, other B-lineage (OBL), CML, normal-BM, and/or CLL in a sample, containing a reference data bank obtainable by comprising

(a) compiling a gene expression profile of a patient sample by determining the expression level at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, and/or 2, and

(b) classifying the gene expression profile by means of a machine learning algorithm.

According to the present invention, the "machine learning algorithm" is a computational-based prediction methodology, also known to the person skilled in the art as "classifier", employed for characterizing a gene expression profile. The signals corresponding to a certain expression level which are obtained by the microarray hybridization are subjected to the algorithm in order to classify the expression profile. Supervised learning involves "training" a classifier to recognize the distinctions among classes and then "testing" the accuracy of the classifier on an independent test set. For new, unknown sample the classifier shall predict into which class the sample belongs.

Preferably, the machine learning algorithm is selected from the group consisting of Weighted Voting, K-Nearest Neighbors, Decision Tree Induction, Support Vector Machines (SVM), and Feed-Forward Neural Networks. Most preferably, the machine learning algorithm is Support Vector Machine, such as polynomial kernel and Gaussian Radial Basis Function-kernel SVM models.

The classification accuracy of a given gene list for a set of microarray experiments is preferably estimated using Support Vector Machines (SVM), because there is evidence that SVM-based prediction slightly outperforms other classification techniques like k-Nearest Neighbors (k-NN). The LIBSVM software package version 2.36 was used (SVM-type: C-SVC, linear kernel (http://www.csie.ntu.edu.tw/~cjlin/libsvm/)). The skilled artisan is furthermore referred to Brown et al., Proc.Natl.Acad.Sci., 2000; 97: 262-267, Furey et al., Bioinformatics. 2000; 16: 906-914, and Vapnik V. Statistical Learning Theory. New York: Wiley, 1998.

In detail, the classification accuracy of a given gene list for a set of microarray experiments can be estimated using Support Vector Machines (SVM) as supervised learning technique. Generally, SVMs are trained using differentially expressed genes which were identified on a subset of the data and then this trained model is employed to assign new samples to those trained groups from a second and different data set. Differentially expressed genes were identified applying ANOVA and t-test-statistics (Welch t-test). Based on identified distinct gene expression signatures respective training sets consisting of 2/3 of cases and test sets with 1/3 of cases to assess classification accuracies are designated. Assignment of cases to

training and test set is randomized and balanced by diagnosis. Based on the training set a Support Vector Machine (SVM) model is built.

According to the present invention, the apparent accuracy, i.e. the overall rate of correct predictions of the complete data set was estimated by 10fold cross validation. This means that the data set was divided into 10 approximately equally sized subsets, an SVM-model was trained for 9 subsets and predictions were generated for the remaining subset. This training and prediction process was repeated 10 times to include predictions for each subset. Subsequently the data set was split into a training set, consisting of two thirds of the samples, and a test set with the remaining one third. Apparent accuracy for the training set was estimated by 10fold cross validation (analogous to apparent accuracy for complete set). A SVM-model of the training set was built to predict diagnosis in the independent test set, thereby estimating true accuracy of the prediction model. This prediction approach was applied both for overall classification (multi-class) and binary classification (diagnosis X => yes or no). For the latter, sensitivity and specificity were calculated:

Sensitivity = (number of positive samples predicted)/(number of true positives)

Specificity = (number of negative samples predicted)/(number of true negatives)

In a preferred embodiment, the reference data bank is backed up on a computational data memory chip which can be inserted in as well as removed from the apparatus of the present invention, e.g. like an interchangeable module, in order to use another data memory chip containing a different reference data bank.

The apparatus of the present invention containing a desired reference data bank can be used in a way such that an unknown sample is, first, subjected to gene expression profiling, e.g. by microarray analysis in a manner as described supra or in the art, and the expression level data obtained by the analysis are, second, fed into the apparatus and compared with the data of the reference data bank obtainable by the above method. For this purpose, the apparatus suitably contains a device for entering the expression level of the data, for example a control panel such as a keyboard. The results, whether and how the data of the unknown sample fit into the reference data bank can be made visible on a provided monitor or display screen and, if desired, printed out on an incorporated of connected printer.

Alternatively, the apparatus of the present invention is equipped with particular appliances suitable for detecting and measuring the expression profile data and, subsequently, proceeding with the comparison with the reference data bank. In this embodiment, the apparatus of the present invention can contain a gripper arm and/or a tray which takes up the microarray containing the hybridized nucleic acids.

In another embodiment, the present invention refers to a reference data bank for distinguishing leukemia subtypes t(15;17), t(8;21), inv(16), inv(3), complex aberrant karyotype (CA), AML-MLL, normal karyotype (NK), AML-other, i.e. trisomy 8, trisomy 11, trisomy 13, monosomy 7, del(5q), del(9q), t(6;9); del(20q) and del(12p) and trisomy 4, ALL-MLL, ALL-Ph+, ALL-t(8;14), T-ALL, other B-lineage (OBL), CML, normal-BM, and/or CLL in a sample obtainable by comprising

(a) compiling a gene expression profile of a patient sample by determining the expression level of at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, and/or 7, and

(b) classifying the gene expression profile by means of a machine learning algorithm.

Preferably, the reference data bank is backed up and/or contained in a computational memory data chip.

The invention is further illustrated in the following Table and Examples, without limiting the scope of the invention:

TABLES 1.1 to 2.78

Tables 1.1 to 2.78 show leukemia subtype analysis of t(15;17), t(8;21), inv(16), inv(3), complex aberrant karyotype (CA), AML-MLL, normal karyotype (NK), AML-other, i.e. trisomy 8, trisomy 11, trisomy 13, monosomy 7, del(5q), del(9q), t(6;9); del(20q) and del(12p) and trisomy 4, ALL-MLL, ALL-Ph+, ALL-t(8;14), T-ALL, other B-lineage (OBL), CML, normal-BM, and/or CLL. The analysed markers are ordered according to their q-values, beginning with the lowest q-values.

For convenience and a better understanding, Tables 1.1 to 2.78 are accompanied with explanatory tables (Table 1.1A to 2.78A) where the numbering and the Affymetrix Id are further defined by other parameters, e.g. gene bank accession number

EXAMPLES

Example 1: General experimental design of the invention and results

So far comprehensive diagnosis of leukemia requires a combination of cytomorphology, immunophenotyping, and genetic methods. We aimed at developing a diagnostic tool based only on gene expression profiling to accurately predict all clinically relevant subtypes of leukemia. Therefore, we analyzed samples from 540 patients at diagnosis using oligonucleotide microarrays representing 33,000 different genes (U133 set, Affymetrix). The following leukemia subtypes were included in this study: 367 AML (20 t(15;17); 25 t(8;21); 25 inv(16); 18 inv(3); 34 complex aberrant karyotype (CA); 30 AML-MLL; 158 normal karyotype (NK); 57 AML-other, i.e. trisomy 8 (n=12), trisomy 11 (n=7), trisomy 13 (n=7), monosomy 7 (n=9), del(5q) (n=7), del(9q) (n=9), t(6;9) (n=3); del(20q) and del(12p) and trisomy 4 one case each); 85 ALL (17 ALL-MLL; 21 ALL-Ph+; 12 ALL-t(8;14); 23 T-ALL; 12 other B-lineage (OBL)), 46 CML, 34 CLL, and 8 bone marrows from healthy volunteers (n-BM). To identify differentially expressed genes we applied ANOVA and t-test-statistics (Welch t-test). To assess the false discovery rate we calculated q values according to Storey et al. (PNAS, 2003). To estimate diagnostic accuracy based on gene expression signatures, we designated a training set consisting of 2/3 of cases and a test set with 1/3 of cases. Assignment of cases to training and test set was randomized and

balanced by diagnosis. Based on the training set we built Support Vector Machine (SVM) models. Classification accuracy was assessed in the independent test set. In the first analysis five main categories AML, ALL, CML, CLL, and n-BM were distinguished in the test set with an accuracy of 96% (177/184 correctly assigned). In a second analysis the following 13 subtypes were included: ALL-MLL, ALL-Ph+, T-ALL, ALL-t(8;14), AML-t(8;21), AML-inv(16), AML-t(15;17), AML-MLL, AML-inv(3), AML-CA, AML-NK, CLL, and CML. 151/154 cases of the test set were correctly assigned (98%). Only two cases with AML-CA and one case with AML-NK were misclassified. In a third analysis n-BM, AML-other and ALL-OBL were added to the 13 subtypes. The accuracy was reduced to 88% (159/180). Categories with 100% sensitivity and specificity each were: n-BM, CLL, CML, ALL-MLL, ALL-t(8;14), AML-t(15;17), and AML-inv(16). AML-other and ALL-OBL, respectively, are considered genetically heterogeneous diseases and are not characterized by a specific gene expression profile. This may have caused the reduced accuracy in the latter SVM analysis. In conclusion, we were able to identify distinct expression profiles for all clinically and prognostically relevant leukemia subtypes based on gene expression data. Sensitivity and specificity were very high when specific leukemia subtypes were included into the analysis. Even the subgroup AML-NK was predicted with high accuracy. Using gene expression profiling as a robust diagnostic tool to correctly subclassify leukemias is a realistic goal and may guide relevant therapeutic consequences in the near future.

Example 2: General materials, methods and definitions of functional annotations

The methods section contains both information on statistical analyses used for identification of differentially expressed genes and detailed annotation data of identified microarray probesets.

Affymetrix Probeset Annotation

All annotation data of GeneChip® arrays are extracted from the NetAffx™ Analysis Center (internet website: www.affymetrix.com). Files for U133 set arrays, including U133A and U133B microarrays are derived from the June 2003 release. The original publication refers to: Liu G, Loraine AE, Shigeta R, Cline M, Cheng J, Valmeekam V, Sun S, Kulp D, Siani-Rose MA. NetAffx: Affymetrix probesets and annotations. Nucleic Acids Res. 2003;31(1):82-6.

The sequence data are omitted due to their large size, and because they do not change, whereas the annotation data are updated periodically, for example new information on chromomal location and functional annotation of the respective gene products. Sequence data are available for download in the NetAffx Download Center (www.affymetrix.com)

Data fields:
In the following section, the content of each field of the data files are described. Microarray probesets, for example found to be differentially expressed between different types of leukemia samples are further described by additional information. The fields are of the following types:

1. GeneChip Array Information
2. Probe Design Information
3. Public Domain and Genomic References

1. GeneChip Array Information

HG-U133 ProbeSet_ID:
HG-U133 ProbeSet_ID describes the probe set identifier. Examples are: 200007_at, 200011_s_at, 200012_x_at.

GeneChip:
The description of the GeneChip probe array name where the respective probeset is represented. Examples are: Affymetrix Human Genome U133A Array or Affymetrix Human Genome U133B Array.

2. Probe Design Information

Sequence Type:
The Sequence Type indicates whether the sequence is an Exemplar, Consensus or Control sequence. An Exemplar is a single nucleotide sequence taken directly from a public database. This sequence could be an mRNA or EST. A Consensus sequence, is a nucleotide sequence assembled by Affymetrix, based on one or more sequence taken from a public database.

Transcript ID:
The cluster identification number with a sub-cluster identifier appended.

Sequence Derived From:
The accession number of the single sequence, or representative sequence on which the probe set is based. Refer to the "Sequence Source" field to determine the database used.

Sequence ID:
For Exemplar sequences: Public accession number or GenBank identifier. For Consensus sequences: Affymetrix identification number or public accession number.

Sequence Source:
The database from which the sequence used to design this probe set was taken. Examples are: GenBank®, RefSeq, UniGene, TIGR (annotations from The Institute for Genomic Research).

3. Public Domain and Genomic References

Most of the data in this section come from LocusLink and UniGene databases, and are annotations of the reference sequence on which the probe set is modeled.

Gene Symbol and Title:
A gene symbol and a short title, when one is available. Such symbols are assigned by different organizations for different species. Affymetrix annotational data come from the UniGene record. There is no indication which species-specific databank was used, but some of the possibilities include for example HUGO: The Human Genome Organization.

MapLocation:
The map location describes the chromosomal location when one is available.

Unigene_Accession:
UniGene accession number and cluster type. Cluster type can be "full length" or "est", or "---" if unknown.

LocusLink:
This information represents the LocusLink accession number.

Full Length Ref. Sequences:
Indicates the references to multiple sequences in RefSeq. The field contains the ID and description for each entry, and there can be multiple entries per probeSet.

Example 3: Sample preparation, processing and data analysis

Method 1:

Microarray analyses were performed utilizing the GeneChip® System (Affymetrix, Santa Clara, USA). Hybridization target preparations were performed according to recommended protocols (Affymetrix Technical Manual). In detail, at time of diagnosis, mononuclear cells were purified by Ficoll-Hypaque density centrifugation. They had been lysed immediately in RLT buffer (Qiagen, Hilden, Germany), frozen, and stored at -80°C from 1 week to 38 months. For gene expression profiling cell lysates of the leukemia samples were thawed, homogenized (QIAshredder, Qiagen), and total RNA was extracted (RNeasy Mini Kit, Qiagen). Subsequently, 5-10 µg total RNA isolated from 1 x 10^7 cells was used as starting material for cDNA synthesis with oligo[$(dT)_{24}$T7promotor]$_{65}$ primer (cDNA Synthesis System, Roche Applied Science, Mannheim, Germany). cDNA products were purified by phenol/chlorophorm/IAA extraction (Ambion, Austin, USA) and acetate/ethanol-precipitated overnight. For detection of the hybridized target nucleic acid biotin-labeled ribonucleotides were incorporated during the following *in vitro* transcription reaction (Enzo BioArray HighYield RNA Transcript Labeling Kit, Enzo Diagnostics). After quantification by spectrophotometric measurements and 260/280 absorbance values assessment for quality control of the purified cRNA (RNeasy Mini Kit, Qiagen), 15 µg cRNA was fragmented by alkaline treatment (200 mM Tris-acetate, pH 8.2/500 mM potassium acetate/150 mM magnesium acetate) and added to the hybridization cocktail sufficient for five hybridizations on standard GeneChip microarrays (300 µl final volume). Washing and staining of the probe arrays was performed according to the recommended Fluidics Station protocol (EukGE-WS2v4). Affymetrix Microarray Suite software (version 5.0.1) extracted fluorescence signal intensities from each feature on the microarrays as detected by confocal laser scanning according to the manufacturer's recommendations.

Expression analysis quality assessment parameters included visiual array inspection of the scanned image for the presence of image artifacts and correct grid alignment for the identification of distinct probe cells as well as both low 3'/5' ratio of housekeeping controls (mean: 1.90 for GAPDH) and high percentage of detection calls (mean: 46.3% present called genes). The 3' to 5' ratio of GAPDH probesets can be used to assess RNA sample and assay quality. Signal values of the 3' probe sets for GAPDH are compared to the Signal values of the corresponding 5' probe set. The ratio of the 3' probe set to the 5' probe set is generally no more than 3.0. A high 3' to 5' ratio may indicate degraded RNA or inefficient synthesis of ds cDNA or biotinylated cRNA (GeneChip® Expression Analysis Technical Manual, www.affymetrix.com). Detection calls are used to determine whether the transcript of a gene is detected (present) or undetected (absent) and were calculated using default parameters of the Microarray Analysis Suite MAS 5.0 software package.

Method 2:

Bone marrow (BM) aspirates are taken at the time of the initial diagnostic biopsy and remaining material is immediately lysed in RLT buffer (Qiagen), frozen and stored at -80 C until preparation for gene expression analysis. For microarray analysis the GeneChip System (Affymetrix, Santa Clara, CA, USA) is used. The targets for GeneChip analysis are prepared according to the current Expression Analysis. Briefly, frozen lysates of the leukemia samples are thawed, homogenized (QIAshredder, Qiagen) and total RNA extracted (RNeasy Mini Kit, Qiagen).Normally 10 ug total RNA isolated from 1 x 107 cells is used as starting material in the subsequent cDNA-Synthesis using Oligo-dT-T7-Promotor Primer (cDNA synthesis Kit, Roche Molecular Biochemicals). The cDNA is purified by phenol-chlorophorm extraction and precipitated with 100% Ethanol over night. For detection of the hybridized target nucleic acid biotin-labeled ribonucleotides are incorporated during the in vitro transcription reaction (Enzo® BioArray™ HighYield™ RNA Transcript Labeling Kit, ENZO). After quantification of the purified cRNA (RNeasy Mini Kit, Qiagen), 15 ug are fragmented by alkaline treatment (200 mM Tris-acetate, pH 8.2, 500 mM potassium acetate, 150 mM magnesium acetate) and added to the hybridization cocktail sufficient for 5 hybridizations on standard GeneChip microarrays. Before expression profiling Test3 Probe Arrays (Affymetrix) are chosen for monitoring of the integrity of the

cRNA. Only labeled cRNA-cocktails which showed a ratio of the messured intensity of the 3' to the 5' end of the GAPDH gene less than 3.0 are selected for subsequent hybridization on HG-U133 probe arrays (Affymetrix). Washing and staining the Probe arrays is performed as described (siehe Affymetrix-Original-Literatur (LOCKHART und LIPSHUTZ). The Affymetrix software (Microarray Suite, Version 4.0.1) extracted fluorescence intensities from each element on the arrays as detected by confocal laser scanning according to the manufacturers recommendations.

Table 1

1. One-Versus-All (OVA)

1.1	ALL_MLL versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	200871_s_at	PSAP	-4.69	1.31E-45	4.49E-42	-1.44	-23.93	10q21-q22
2	204949_at	ICAM3	-8.98	8.00E-66	2.29E-61	-1.33	-23.57	19p13.3-p13.2
3	217800_s_at	NDFIP1	-7.80	2.52E-40	3.60E-37	-1.40	-22.79	5q31.3
4	202382_s_at	GNPI	-10.47	1.41E-45	4.49E-42	-1.30	-21.95	5q21
5	227353_at	EVER2	-3.80	4.54E-29	1.43E-26	-1.30	-20.02	17q25.3
6	224918_x_at	MGST1	-26.96	5.22E-54	7.46E-50	-1.06	-18.96	12p12.3-p12.1
7	204852_s_at	PTPN7	-3.58	2.48E-24	4.41E-22	-1.29	-18.96	1q32.1
8	218486_at		-13.86	2.02E-53	1.92E-49	-1.04	-18.71	
9	218942_at	FLJ22055	-6.87	3.54E-28	9.74E-26	-1.20	-18.65	12q13.13
10	202853_s_at	RYK	-4.84	1.07E-23	1.76E-21	-1.27	-18.60	3q22
11	218831_s_at	FCGRT	-8.33	3.72E-35	2.73E-32	-1.11	-18.40	19q13.3
12	225782_at	LOC253827	-20.15	3.28E-52	2.34E-48	-1.02	-18.40	12q14.1
13	231736_x_at	MGST1	-21.12	2.30E-50	1.32E-46	-1.00	-18.01	12p12.3-p12.1
14	200866_s_at	PSAP	-4.22	1.41E-39	1.83E-36	-1.05	-17.99	10q21-q22
15	200953_s_at	CCND2	-4.80	8.21E-46	3.35E-42	-1.00	-17.72	12p13
16	217967_s_at	C1orf24	-6.05	3.14E-43	6.92E-40	-1.01	-17.70	1q25
17	210024_s_at	UBE2E3	-5.80	7.63E-23	1.14E-20	-1.20	-17.62	2q32.1
18	202788_at	MAPKAPK3	-2.77	1.09E-31	4.97E-29	-1.08	-17.56	3p21.3
19	225789_at	CENTG3	-4.34	3.82E-20	4.12E-18	-1.24	-17.32	7q36.1
20	201494_at	PRCP	-2.83	4.16E-31	1.80E-28	-1.06	-17.27	11q14
21	219013_at	GALNT11	-4.85	4.62E-28	1.23E-25	-1.09	-17.24	7q34-q36
22	225637_at	FLJ20186	-8.53	6.63E-44	1.58E-40	-0.97	-17.10	16q24.3
23	225790_at	LOC253827	-20.03	4.39E-47	2.09E-43	-0.95	-17.10	12q14.1
24	204446_s_at	ALOX5	-7.63	7.02E-42	1.34E-38	-0.97	-17.04	10q11.2
25	204563_at	SELL	-6.10	8.12E-41	1.22E-37	-0.96	-16.75	1q23-q25
26	203591_s_at	CSF3R	-7.86	2.25E-44	5.86E-41	-0.93	-16.68	1p35-p34.3
27	203949_at	MPO	-10.32	5.42E-41	9.11E-38	-0.95	-16.62	17q23.1
28	203948_s_at	MPO	-18.02	1.19E-44	3.39E-41	-0.91	-16.47	17q23.1
29	213116_at	NEK3	-4.07	5.46E-24	9.30E-22	-1.07	-16.37	13q14.13
30	203973_s_at	CEBPD	-6.99	4.38E-33	2.41E-30	-0.95	-16.12	8p11.2-p11.1
31	200602_at	APP	-10.63	2.84E-42	5.80E-39	-0.89	-16.01	21q21.3
32	204214_s_at	RAB32	-4.61	1.16E-29	3.89E-27	-0.96	-15.91	6q24.2
33	224448_s_at	MGC14833	-3.23	2.47E-30	9.96E-28	-0.95	-15.76	6p21.31
34	206120_at	CD33	-27.98	1.99E-41	3.56E-38	-0.88	-15.73	19q13.3
35	219191_s_at	BIN2	-7.62	2.60E-29	8.46E-27	-0.95	-15.69	12q13
36	220307_at	CD244	-5.49	3.28E-35	2.47E-32	-0.90	-15.64	1q23.1
37	201425_at	ALDH2	-5.98	9.46E-39	1.18E-35	-0.88	-15.64	12q24.2
38	204487_s_at	KCNQ1	-15.82	1.56E-36	1.54E-33	-0.89	-15.58	11p15.5
39	205639_at	AOAH	-10.01	2.09E-38	2.49E-35	-0.88	-15.56	7p14-p12

Table 1

40	210424_s_at	GOLGIN-67	-5.32	1.22E-32	6.25E-30	-0.91	-15.54	15q11.2
41	223046_at	EGLN1	-4.24	1.81E-24	3.23E-22	-0.99	-15.53	1q42.1
42	212593_s_at	PDCD4	-3.26	3.68E-25	7.26E-23	-0.98	-15.52	10q24
43	201462_at	KIAA0193	-10.60	6.89E-41	1.09E-37	-0.86	-15.51	7p14.3-p14.1
44	228058_at	LOC124220	-8.52	4.68E-38	5.35E-35	-0.88	-15.50	16p13.3
45	218910_at	FLJ10375	-10.04	7.34E-40	9.99E-37	-0.85	-15.28	3p21.32
46	214181_x_at	LST1	-5.17	3.49E-34	2.27E-31	-0.88	-15.27	6p21.3
47	204661_at	CDW52	-9.95	2.32E-36	2.07E-33	-0.86	-15.14	1p36
48	227001_at		-3.56	7.90E-22	1.03E-19	-1.00	-15.13	
49	204122_at	TYROBP	-5.71	1.11E-37	1.17E-34	-0.85	-15.11	19q13.1
50	214172_x_at	RYK	-3.21	7.53E-16	4.77E-14	-1.17	-15.05	3q22
1.2	ALL_Ph+ versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	234107_s_at	HARS2	-3.71	2.79E-39	8.04E-35	-1.09	-18.35	20p11.23
2	205020_s_at	ARL4	-3.73	7.65E-26	1.96E-22	-0.88	-14.28	7p21-p15.3
3	201462_at	KIAA0193	-8.11	2.94E-35	4.24E-31	-0.80	-14.27	7p14.3-p14.1
4	218404_at	SNX10	-4.49	1.18E-26	3.77E-23	-0.87	-14.18	7p15.2
5	224839_s_at	GPT2	-11.60	1.24E-34	1.19E-30	-0.78	-13.92	16q12.1
6	218718_at	PDGFC	-7.17	6.00E-34	4.32E-30	-0.76	-13.69	4q32
7	203955_at	KIAA0649	-5.68	7.28E-32	4.20E-28	-0.78	-13.68	9q34.3
8	204362_at	SCAP2	-4.98	1.11E-27	4.57E-24	-0.81	-13.61	7p21-p15
9	224918_x_at	MGST1	-6.75	4.62E-24	7.00E-21	-0.79	-12.92	12p12.3-p12.1
10	231736_x_at	MGST1	-6.49	1.29E-25	2.85E-22	-0.77	-12.89	12p12.3-p12.1
11	219452_at	LOC64174	-10.71	1.02E-29	4.91E-26	-0.71	-12.69	16q22.1
12	225639_at	SCAP2	-4.73	1.03E-23	1.35E-20	-0.76	-12.56	7p21-p15
13	226794_at	STXBP5	-4.21	1.53E-24	2.45E-21	-0.74	-12.44	6q24.3
14	216899_s_at	SCAP2	-4.04	3.41E-27	1.23E-23	-0.71	-12.37	7p21-p15
15	204214_s_at	RAB32	-3.56	2.08E-19	1.28E-16	-0.81	-12.37	6q24.2
16	204072_s_at	13CDNA73	-4.51	8.15E-26	1.96E-22	-0.71	-12.26	13q12.3
17	228642_at		-3.46	9.77E-25	1.66E-21	-0.72	-12.25	
18	219229_at	SLC21A11	-4.83	3.25E-18	1.54E-15	-0.81	-12.09	15q26
19	227266_s_at		-4.00	4.32E-23	5.41E-20	-0.72	-11.99	
20	221080_s_at	FLJ22757	-1.81	1.78E-14	4.04E-12	-0.94	-11.96	19p13.3
21	204361_s_at	SCAP2	-4.95	3.53E-21	2.99E-18	-0.74	-11.93	7p21-p15
22	205645_at	REPS2	-5.66	1.79E-25	3.53E-22	-0.68	-11.93	Xp22.22
23	202295_s_at	CTSH	-4.50	3.24E-26	9.35E-23	-0.67	-11.90	15q24-q25
24	223501_at		-3.87	1.44E-21	1.38E-18	-0.72	-11.82	
25	203373_at	SOCS2	4.48	3.39E-12	3.73E-10	1.18	11.81	12q
26	223703_at	CDA017	-3.03	1.40E-21	1.38E-18	-0.72	-11.79	10q23.1
27	202746_at	ITM2A	-4.64	8.63E-25	1.55E-21	-0.68	-11.78	Xq13.3-Xq21.2
28	208702_x_at	APLP2	-3.52	5.19E-19	2.88E-16	-0.75	-11.75	11q24
29	214875_x_at	APLP2	-3.52	1.55E-20	1.18E-17	-0.72	-11.67	11q24

Table 1

30	223502_s_at	TNFSF13B	-3.75	8.19E-20	5.49E-17	-0.73	-11.62	13q32-34
31	211404_s_at	APLP2	-3.26	3.96E-18	1.84E-15	-0.75	-11.54	11q24
32	204167_at	BTD	-4.32	6.90E-21	5.52E-18	-0.70	-11.50	3p25
33	201384_s_at	M17S2	-2.20	6.75E-17	2.56E-14	-0.77	-11.40	17q21.1
34	219919_s_at	SSH-3	-5.41	1.84E-25	3.53E-22	-0.63	-11.38	11q13.1
35	227947_at		-4.28	2.51E-19	1.45E-16	-0.71	-11.33	
36	242282_at		-2.01	1.78E-20	1.31E-17	-0.68	-11.26	
37	202747_s_at	ITM2A	-4.80	6.39E-23	7.67E-20	-0.65	-11.25	Xq13.3-Xq21.2
38	217963_s_at	NGFRAP1	-6.85	6.66E-24	9.60E-21	-0.63	-11.18	Xq22.1
39	220326_s_at	FLJ10357	-2.94	7.85E-21	6.12E-18	-0.67	-11.18	14q11.1
40	211795_s_at	FYB	-3.85	3.41E-21	2.98E-18	-0.65	-11.07	5p13.1
41	51192_at	SSH-3	-2.73	2.19E-14	4.86E-12	-0.81	-11.02	11q13.1
42	239135_at		-4.00	1.59E-21	1.48E-18	-0.64	-11.01	
43	225782_at	LOC253827	-7.35	4.09E-16	1.36E-13	-0.74	-10.99	12q14.1
44	228970_at		-1.69	9.77E-17	3.66E-14	-0.72	-10.98	
45	212934_at	LOC137886	-2.55	3.09E-16	1.05E-13	-0.74	-10.96	8q11.23
46	227230_s_at	KIAA1211	-6.11	8.66E-24	1.19E-20	-0.61	-10.91	4q12
47	227425_at		-2.44	1.38E-19	8.86E-17	-0.66	-10.90	
48	218094_s_at	C20orf35	-2.93	2.50E-18	1.21E-15	-0.68	-10.87	20q13.11
49	225386_s_at	LOC92906	-6.39	2.41E-17	9.93E-15	-0.69	-10.84	2p22.2
50	223635_s_at	SSBP3	-2.05	4.42E-21	3.64E-18	-0.63	-10.83	1p32.3
1.3	ALL_T-lineage versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	200742_s_at	CLN2	-4.55	6.96E-44	2.18E-40	-1.22	-20.51	11p15
2	203555_at	PTPN18	-4.79	1.52E-41	2.78E-38	-1.19	-19.93	2q21.1
3	210982_s_at	HLA-DRA	-13.87	1.28E-52	1.41E-48	-1.05	-18.75	6p21.3
4	213521_at		-3.46	9.17E-34	4.38E-31	-1.16	-18.64	
5	208894_at	HLA-DRA	-13.65	1.17E-52	1.41E-48	-1.04	-18.62	6p21.3
6	217478_s_at	HLA-DMA	-7.59	3.21E-48	2.35E-44	-1.02	-18.08	6p21.3
7	200696_s_at	GSN	-5.91	3.22E-39	3.08E-36	-1.03	-17.51	9q33
8	202241_at	C8FW	-6.10	2.14E-40	2.46E-37	-1.02	-17.45	8q24.13
9	203799_at	BIMLEC	-7.89	3.55E-41	5.56E-38	-1.01	-17.45	2q24.2
10	226459_at	FLJ35564	-4.25	3.03E-29	7.74E-27	-1.11	-17.43	10q23.33
11	205640_at	ALDH3B1	-9.58	9.29E-42	2.04E-38	-1.00	-17.31	11q13
12	215193_x_at	HLA-DRB1	-9.23	3.55E-44	1.30E-40	-0.98	-17.28	6p21.3
13	211991_s_at	HLA-DPA1	-13.54	1.96E-46	1.08E-42	-0.95	-17.10	6p21.3
14	223696_at		-9.13	2.44E-41	4.12E-38	-0.98	-17.07	
15	200743_s_at	CLN2	-3.26	2.64E-22	2.14E-20	-1.21	-17.00	11p15
16	216041_x_at	GRN	-5.97	7.12E-39	6.51E-36	-0.98	-16.87	17q21.32
17	223703_at	CDA017	-4.50	1.33E-45	5.83E-42	-0.94	-16.86	10q23.1
18	217984_at	RNASE6PL	-2.56	1.85E-25	2.47E-23	-1.12	-16.80	6q27
19	200678_x_at	GRN	-5.60	7.23E-36	4.18E-33	-0.98	-16.64	17q21.32

Table 1

20	203949_at	MPO	-9.73	1.21E-41	2.41E-38	-0.93	-16.48	17q23.1
21	204122_at	TYROBP	-8.16	2.33E-43	6.41E-40	-0.91	-16.37	19q13.1
22	212335_at	GNS	-3.95	9.33E-38	7.07E-35	-0.95	-16.34	12q14
23	207571_x_at	C1orf38	-6.10	3.38E-28	7.29E-26	-1.02	-16.15	1p35.2
24	211284_s_at	GRN	-6.27	2.70E-38	2.20E-35	-0.93	-16.12	17q21.32
25	222698_s_at	IMPACT	-3.52	3.00E-23	2.70E-21	-1.09	-16.09	18q11.2-q12.1
26	223553_s_at	FLJ22570	-4.19	2.69E-35	1.48E-32	-0.93	-15.94	5q35.3
27	200808_s_at	ZYX	-3.97	3.41E-32	1.21E-29	-0.96	-15.93	7q32
28	214196_s_at	CLN2	-4.56	5.40E-33	2.26E-30	-0.95	-15.92	11p15
29	203028_s_at	CYBA	-4.34	3.76E-33	1.62E-30	-0.95	-15.90	16q24
30	203948_s_at	MPO	-15.53	4.97E-42	1.21E-38	-0.88	-15.88	17q23.1
31	204670_x_at	HLA-DRB5	-5.65	7.92E-30	2.26E-27	-0.97	-15.86	6p21.3
32	211990_at	HLA-DPA1	-5.63	2.63E-23	2.39E-21	-1.07	-15.85	6p21.3
33	208306_x_at	HLA-DRB4	-6.80	6.10E-31	1.97E-28	-0.96	-15.85	6p21.3
34	218217_at	RISC	-5.85	5.61E-41	7.71E-38	-0.88	-15.80	17q23.1
35	231736_x_at	MGST1	-11.45	5.62E-40	5.88E-37	-0.89	-15.76	12p12.3-p12.1
36	224918_x_at	MGST1	-11.37	4.15E-37	2.85E-34	-0.90	-15.67	12p12.3-p12.1
37	206111_at	RNASE2	-5.92	1.09E-32	4.26E-30	-0.93	-15.62	14q24-q31
38	201137_s_at	HLA-DPB1	-6.95	2.04E-34	1.04E-31	-0.91	-15.61	6p21.3
39	209166_s_at	MAN2B1	-2.50	7.07E-27	1.20E-24	-0.99	-15.60	19cen-q13.1
40	201887_at	IL13RA1	-6.31	2.24E-40	2.46E-37	-0.87	-15.60	Xq24
41	209473_at	ENTPD1	-4.99	4.42E-41	6.48E-38	-0.87	-15.59	10q24
42	225059_at	AGTRAP	-7.63	2.29E-39	2.29E-36	-0.88	-15.56	1p36.21
43	225286_at		-5.12	3.13E-27	5.79E-25	-0.97	-15.51	
44	226190_at		-4.03	4.31E-35	2.25E-32	-0.90	-15.51	
45	209312_x_at	HLA-DRB1	-5.99	1.33E-28	3.08E-26	-0.96	-15.49	6p21.3
46	214575_s_at	AZU1	-23.06	1.08E-40	1.32E-37	-0.86	-15.48	19p13.3
47	219013_at	GALNT11	-4.31	4.31E-25	5.29E-23	-1.00	-15.48	7q34-q36
48	220416_at	KIAA1939	-13.11	8.28E-41	1.07E-37	-0.86	-15.48	15q15.3
49	223158_s_at	NEK6	-3.93	1.75E-25	2.35E-23	-0.99	-15.43	9q33.3-q34.11
50	210613_s_at	SYNGR1	-5.84	1.10E-26	1.81E-24	-0.97	-15.35	22q13.1
1.4	ALL_t(8;14) versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	231982_at		-15.62	1.24E-43	2.48E-39	-0.97	-17.11	
2	211709_s_at	SCGF	-7.06	1.69E-29	5.62E-26	-0.96	-16.01	19q13.3
3	226869_at		-9.09	2.77E-13	5.47E-11	-1.08	-13.91	
4	215111_s_at	TSC22	-4.58	8.80E-30	3.52E-26	-0.79	-13.69	13q14
5	206674_at	FLT3	-11.37	9.71E-32	9.70E-28	-0.73	-13.15	13q12
6	215537_x_at	DDAH2	-4.90	2.43E-17	1.24E-14	-0.87	-13.09	6p21.3
7	209160_at	AKR1C3	-7.74	3.88E-30	1.94E-26	-0.73	-13.04	10p15-p14
8	213589_s_at	LOC284208	-12.10	1.69E-30	1.13E-26	-0.71	-12.77	17q25.3
9	201028_s_at	CD99	-3.71	4.52E-25	8.22E-22	-0.75	-12.74	Xp22.32

Table 1

10	201029_s_at	CD99	-3.03	1.81E-13	3.73E-11	-0.92	-12.51	Xp22.32
11	215116_s_at	DNM1	-6.08	1.15E-28	3.29E-25	-0.70	-12.44	9q34
12	225306_s_at	C14orf69	-4.39	3.84E-15	1.13E-12	-0.85	-12.40	14q32.32
13	205131_x_at	SCGF	-10.46	9.49E-28	2.11E-24	-0.70	-12.39	19q13.3
14	201825_s_at	CGI-49	-2.62	3.68E-17	1.75E-14	-0.80	-12.29	1q44
15	209199_s_at	MEF2C	-5.89	5.11E-28	1.28E-24	-0.69	-12.29	5q14
16	202747_s_at	ITM2A	-6.89	1.43E-23	2.19E-20	-0.72	-12.26	Xq13.3-Xq21.2
17	204798_at	MYB	-3.63	3.51E-13	6.85E-11	-0.90	-12.21	6q22-q23
18	202768_at	FOSB	-4.53	1.84E-17	9.92E-15	-0.78	-12.15	19q13.32
19	219654_at	PTPLA	-5.46	9.69E-26	1.94E-22	-0.69	-12.04	10p14-p13
20	214909_s_at	DDAH2	-3.39	5.58E-17	2.53E-14	-0.78	-12.00	6p21.3
21	230127_at		-5.50	2.49E-18	1.66E-15	-0.74	-11.87	
22	202708_s_at	HIST2H2BE	-3.37	1.47E-19	1.54E-16	-0.73	-11.86	1q21-q23
23	213541_s_at	ERG	-4.13	8.42E-18	4.95E-15	-0.75	-11.85	21q22.3
24	209360_s_at	RUNX1	-5.43	4.57E-14	1.13E-11	-0.82	-11.77	21q22.3
25	212442_s_at	LOC253782	-3.65	1.36E-11	2.08E-09	-0.91	-11.65	2q31.1
26	229307_at		-3.94	6.06E-15	1.70E-12	-0.78	-11.61	
27	201162_at	IGFBP7	-5.69	2.37E-16	8.95E-14	-0.74	-11.51	4q12
28	219201_s_at	TWSG1	-5.30	2.95E-19	2.56E-16	-0.70	-11.49	18p11.3
29	202262_x_at	DDAH2	-3.71	1.52E-11	2.28E-09	-0.86	-11.26	6p21.3
30	201564_s_at	FSCN1	-7.38	2.93E-22	3.90E-19	-0.64	-11.16	7p22
31	219871_at	FLJ13197	-4.24	9.23E-17	4.01E-14	-0.70	-11.12	4p14
32	201826_s_at	CGI-49	-2.15	1.68E-15	5.50E-13	-0.71	-11.04	1q44
33	201324_at	EMP1	-9.80	3.92E-24	6.53E-21	-0.61	-11.02	12p12.3
34	200665_s_at	SPARC	-6.99	1.13E-18	8.36E-16	-0.66	-10.93	5q31.3-q32
35	224710_at	RAB34	-4.78	2.37E-11	3.44E-09	-0.82	-10.80	17q11.1
36	224851_at		-3.95	1.66E-19	1.66E-16	-0.63	-10.72	
37	208634_s_at	MACF1	-2.82	8.77E-13	1.54E-10	-0.75	-10.72	1p32-p31
38	210612_s_at	SYNJ2	-4.93	2.69E-16	9.96E-14	-0.67	-10.70	6q25.3
39	201325_s_at	EMP1	-15.76	2.03E-22	2.90E-19	-0.58	-10.51	12p12.3
40	219634_at	C4ST	-2.98	1.11E-10	1.35E-08	-0.82	-10.50	12q
41	206067_s_at	WT1	-30.72	3.83E-22	4.78E-19	-0.58	-10.45	11p13
42	209530_at	CACNB3	-2.66	2.18E-15	7.01E-13	-0.66	-10.38	12q13
43	202746_at	ITM2A	-4.18	4.20E-16	1.50E-13	-0.64	-10.37	Xq13.3-Xq21.2
44	209267_s_at	BIGM103	-2.68	1.61E-11	2.40E-09	-0.74	-10.26	4q22-q24
45	243000_at		-5.18	2.89E-19	2.56E-16	-0.59	-10.24	
46	225962_at	NIN283	-10.30	3.60E-21	4.22E-18	-0.57	-10.21	16q22.3
47	223383_at	NIN283	-4.91	1.23E-11	1.91E-09	-0.73	-10.21	16q22.3
48	210613_s_at	SYNGR1	-3.96	3.86E-10	4.36E-08	-0.80	-10.13	22q13.1
49	210298_x_at	FHL1	-6.53	3.66E-19	3.05E-16	-0.58	-10.13	Xq26
50	212959_s_at	MGC4170	-2.69	4.27E-11	6.00E-09	-0.73	-10.02	12q23.3
1.5	AML_MLL versus rest							

Table 1

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	204951_at	ARHH	-5.93	3.09E-38	4.88E-34	-0.85	-15.16	4p13
2	233849_s_at	ARHGAP5	-7.32	1.26E-31	3.18E-28	-0.84	-14.36	14q12
3	226517_at	BCAT1	-7.88	9.15E-36	7.24E-32	-0.79	-14.24	12pter-q12
4	220306_at	FLJ20202	-3.90	1.41E-31	3.18E-28	-0.82	-14.10	1p11.1
5	214022_s_at	MGC27165	-3.88	3.34E-30	5.86E-27	-0.79	-13.60	14
6	208650_s_at	CD24	-10.89	1.93E-33	1.02E-29	-0.75	-13.55	6q21
7	202746_at	ITM2A	-7.35	2.15E-32	6.81E-29	-0.76	-13.55	Xq13.3-Xq21.2
8	266_s_at	CD24	-7.99	1.88E-32	6.81E-29	-0.74	-13.33	6q21
9	216379_x_at	KIAA1919	-6.33	9.18E-31	1.82E-27	-0.75	-13.27	6q22
10	203544_s_at	STAM	-3.00	8.34E-25	4.00E-22	-0.81	-13.08	10p14-p13
11	200602_at	APP	-7.59	1.15E-27	8.66E-25	-0.76	-13.04	21q21.3
12	215785_s_at	CYFIP2	-4.43	1.13E-25	6.64E-23	-0.78	-12.96	5q34
13	209771_x_at	CD24	-5.70	2.28E-28	2.52E-25	-0.74	-12.88	6q21
14	214651_s_at	HOXA9	6.94	4.74E-15	2.52E-13	1.32	12.84	7p15-p14
15	202747_s_at	ITM2A	-7.69	3.61E-29	5.19E-26	-0.72	-12.76	Xq13.3-Xq21.2
16	236198_at		-7.42	9.78E-30	1.55E-26	-0.71	-12.64	
17	207734_at	LAX	-2.48	2.39E-28	2.52E-25	-0.72	-12.61	1q32.1
18	212758_s_at	TCF8	-4.36	2.82E-27	2.03E-24	-0.72	-12.53	10p11.2
19	201601_x_at	MGC27165	-4.36	2.34E-28	2.52E-25	-0.70	-12.43	14
20	228029_at	KIAA1982	-5.37	2.03E-28	2.52E-25	-0.70	-12.43	4p16.3
21	211137_s_at	ATP2C1	-1.97	5.29E-27	3.64E-24	-0.71	-12.42	3q21-q24
22	208657_s_at	MSF	-3.27	2.78E-28	2.75E-25	-0.70	-12.40	17q25
23	212764_at	TCF8	-5.40	3.16E-28	2.94E-25	-0.69	-12.33	10p11.2
24	215082_at		-2.00	9.82E-28	7.77E-25	-0.70	-12.31	
25	214643_x_at	BIN1	-3.31	1.11E-22	3.32E-20	-0.76	-12.31	2q14
26	217936_at		-3.36	2.33E-22	6.14E-20	-0.77	-12.27	
27	204881_s_at	UGCG	-3.94	1.06E-26	6.97E-24	-0.70	-12.21	9q31
28	214439_x_at	BIN1	-3.05	3.84E-22	9.80E-20	-0.76	-12.17	2q14
29	200965_s_at	ABLIM1	-5.65	3.90E-28	3.43E-25	-0.67	-12.12	10q25
30	206761_at	TACTILE	-9.25	7.09E-28	5.90E-25	-0.68	-12.10	3q13.13
31	210875_s_at	TCF8	-4.53	2.24E-25	1.18E-22	-0.70	-12.08	10p11.2
32	213737_x_at		2.27	6.42E-15	3.26E-13	1.08	12.01	
33	220104_at	ZAP	-2.64	3.06E-23	1.01E-20	-0.72	-11.96	7q34
34	213549_at	PRO2730	-3.07	7.54E-26	4.59E-23	-0.67	-11.85	3p21.31
35	220999_s_at	PRO1331	-3.76	1.10E-26	6.97E-24	-0.66	-11.78	5q33.3
36	226765_at	SPTBN1	-2.35	1.14E-19	1.76E-17	-0.76	-11.67	2p21
37	212912_at		-3.62	4.13E-24	1.72E-21	-0.68	-11.65	
38	210201_x_at	BIN1	-2.55	2.83E-21	5.81E-19	-0.72	-11.63	2q14
39	214953_s_at	APP	-4.76	3.77E-21	7.36E-19	-0.72	-11.61	21q21.3
40	209447_at	SYNE1	-3.88	1.86E-25	1.01E-22	-0.65	-11.51	6q25
41	243888_at		-3.20	2.95E-24	1.29E-21	-0.66	-11.51	
42	230006_s_at	DKFZp313A2432	-3.00	5.75E-23	1.82E-20	-0.68	-11.49	11p14.2
43	225706_at	GLCCI1	-2.98	6.28E-24	2.42E-21	-0.66	-11.47	7p22.1
44	225285_at		-6.18	1.52E-22	4.35E-20	-0.68	-11.44	
45	225912_at	TP53INP1	-3.74	9.49E-25	4.41E-22	-0.65	-11.42	8q22

46	214390_s_at	BCAT1	-5.87	1.15E-24	5.18E-22	-0.65	-11.42	12pter-q12
47	212071_s_at	SPTBN1	-2.69	5.08E-18	5.66E-16	-0.77	-11.41	2p21
48	236293_at		-4.77	1.85E-25	1.01E-22	-0.63	-11.38	
49	209772_s_at	CD24	-12.97	2.42E-25	1.24E-22	-0.63	-11.38	6q21
50	201906_s_at	HYA22	-3.93	3.02E-24	1.29E-21	-0.65	-11.36	3p21.3
1.6	AML_inv(16) versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	202370_s_at	CBFB	-2.62	6.35E-36	1.93E-32	-1.18	-19.07	16q22.1
2	223471_at	RAB3IP	-3.77	3.17E-31	2.89E-28	-1.06	-17.08	
3	212463_at		-5.74	4.28E-45	7.79E-41	-0.95	-16.98	
4	201669_s_at	MARCKS	-12.31	4.26E-43	3.88E-39	-0.89	-16.07	6q22.2
5	218414_s_at	NUDE1	-2.28	5.37E-27	2.58E-24	-1.03	-16.00	16p13.11
6	200985_s_at	CD59	-8.79	3.32E-40	2.02E-36	-0.87	-15.58	11p13
7	204198_s_at	RUNX3	-5.12	3.13E-31	2.89E-28	-0.93	-15.47	1p36
8	227567_at		-4.69	1.23E-34	2.49E-31	-0.89	-15.31	
9	201811_x_at	SH3BP5	-5.39	3.34E-34	5.53E-31	-0.87	-15.09	3p24.3
10	204197_s_at	RUNX3	-3.47	5.77E-35	1.50E-31	-0.87	-15.04	1p36
11	222786_at	C4S-2	-2.85	2.80E-32	3.19E-29	-0.88	-14.91	7p22
12	201810_s_at	SH3BP5	-4.01	5.48E-37	2.49E-33	-0.82	-14.67	3p24.3
13	200984_s_at	CD59	-3.96	1.61E-34	2.93E-31	-0.82	-14.40	11p13
14	228497_at	FLIPT1	-5.80	5.09E-36	1.85E-32	-0.79	-14.24	1p13.1
15	213002_at	MARCKS	-3.35	1.00E-34	2.28E-31	-0.79	-14.09	6q22.2
16	225706_at	GLCCI1	-4.09	4.30E-33	5.60E-30	-0.80	-14.07	7p22.1
17	225055_at	DKFZp667M2411	-4.30	2.47E-30	1.96E-27	-0.82	-14.06	17q11.2
18	227856_at	FLJ39370	-5.51	1.89E-29	1.28E-26	-0.82	-13.96	4q25
19	201670_s_at	MARCKS	-15.19	4.62E-34	7.01E-31	-0.76	-13.75	6q22.2
20	232611_at	LOC92497	-6.81	6.29E-34	8.82E-31	-0.76	-13.71	12q23.2
21	218795_at	ACP6	-3.80	3.96E-26	1.44E-23	-0.83	-13.60	1q21
22	224952_at	DKFZP564D166	-3.75	2.72E-23	7.29E-21	-0.86	-13.55	17q23.3
23	213353_at	ABCA5	-3.92	4.60E-28	2.62E-25	-0.79	-13.42	17q24.3
24	225897_at		-6.97	1.48E-32	1.80E-29	-0.74	-13.33	
25	201690_s_at	TPD52	-5.18	1.57E-31	1.66E-28	-0.74	-13.26	8q21
26	226352_at		-5.57	1.64E-31	1.66E-28	-0.74	-13.25	
27	200983_x_at	CD59	-6.80	3.43E-31	2.98E-28	-0.72	-13.01	11p13
28	218456_at	EEG1	-3.46	1.29E-29	9.01E-27	-0.74	-12.98	12p11
29	205760_s_at	OGG1	-2.60	4.51E-23	1.11E-20	-0.81	-12.97	3p26.2
30	235165_at		-6.66	1.50E-22	3.38E-20	-0.80	-12.77	
31	213241_at		-5.89	1.73E-30	1.43E-27	-0.71	-12.77	
32	210425_x_at	GOLGIN-67	-3.54	6.91E-29	4.20E-26	-0.72	-12.67	15q11.2
33	228155_at	MGC4248	-4.09	4.62E-30	3.51E-27	-0.70	-12.65	10q22.3
34	202085_at	TJP2	-4.52	5.72E-28	3.16E-25	-0.72	-12.61	9q13-q21
35	226884_at	KIAA1497	-9.67	8.52E-30	6.21E-27	-0.70	-12.58	3p26.2

Table 1

36	213908_at		-5.40	4.00E-29	2.52E-26	-0.70	-12.53	
37	218477_at	PTD011	-2.60	8.52E-22	1.71E-19	-0.78	-12.50	6p12.1
38	209406_at	BAG2	-3.44	7.67E-27	3.41E-24	-0.72	-12.50	6p12.3-p11.2
39	204160_s_at	ENPP4	-7.47	3.92E-29	2.52E-26	-0.70	-12.49	6p12.3
40	229202_at		-4.58	2.03E-28	1.19E-25	-0.69	-12.38	
41	218872_at	TSC	-3.50	2.99E-26	1.14E-23	-0.71	-12.35	12q24.22
42	218927_s_at	C4S-2	-4.35	2.21E-22	4.75E-20	-0.76	-12.34	7p22
43	203973_s_at	CEBPD	2.63	1.67E-13	7.18E-12	1.13	12.23	8p11.2-p11.1
44	230894_s_at		-8.50	2.09E-27	1.11E-24	-0.69	-12.22	
45	223044_at	SLC11A3	-7.41	3.54E-27	1.79E-24	-0.69	-12.21	2q32
46	209447_at	SYNE1	-4.96	1.05E-26	4.55E-24	-0.69	-12.19	6q25
47	201689_s_at	TPD52	-5.86	1.82E-26	7.52E-24	-0.69	-12.16	8q21
48	200665_s_at	SPARC	4.91	3.73E-12	1.15E-10	1.48	12.11	5q31.3-q32
49	215785_s_at	CYFIP2	-3.50	1.38E-22	3.14E-20	-0.73	-12.07	5q34
50	227525_at	GLCCI1	-4.81	2.80E-26	1.11E-23	-0.69	-12.07	7p22.1
1.7	AML_inv(3) versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	210115_at	RPL39L	-7.48	1.35E-41	2.92E-37	-0.87	-15.68	3q27
2	212318_at	TRN-SR	-2.41	2.80E-19	3.77E-16	-1.06	-15.18	7q32.2
3	226123_at	LOC286180	-4.56	1.13E-25	4.08E-22	-0.92	-14.88	8q12.1
4	218829_s_at	KIAA1416	-3.06	1.78E-27	7.68E-24	-0.90	-14.76	8q12.1
5	204921_at	GAS8	-2.81	4.43E-29	2.39E-25	-0.85	-14.36	16q24.3
6	204301_at	KIAA0711	-6.66	2.01E-34	2.16E-30	-0.78	-13.99	8p23.2
7	203421_at	PIG11	-5.39	3.01E-34	2.16E-30	-0.78	-13.94	11p11.2
8	226685_at		-2.28	2.20E-24	6.80E-21	-0.70	-12.02	
9	244166_at		-5.32	8.66E-24	2.34E-20	-0.70	-11.97	
10	205248_at	C21orf5	-2.07	2.54E-17	2.11E-14	-0.78	-11.82	21q22.2
11	214141_x_at	SFRS7	-1.64	1.51E-14	4.18E-12	-0.81	-11.37	2p22.1
12	230044_at		-2.85	1.66E-13	3.35E-11	-0.83	-11.23	
13	226789_at		-2.63	2.65E-17	2.12E-14	-0.71	-11.13	
14	203467_at	PMM1	-3.02	2.57E-14	6.59E-12	-0.76	-10.94	22q13.2
15	227172_at	LOC89894	-1.64	2.96E-15	1.10E-12	-0.73	-10.92	12q24.13
16	203746_s_at	HCCS	-1.45	4.89E-19	6.21E-16	-0.65	-10.80	Xp22.3
17	227929_at		-7.69	1.53E-22	3.31E-19	-0.60	-10.73	
18	203046_s_at	TIMELESS	-2.22	2.90E-14	7.27E-12	-0.74	-10.70	12q12-q13
19	214475_x_at	CAPN3	-8.27	1.29E-21	2.54E-18	-0.60	-10.60	15q15.1-q21.1
20	221558_s_at	LEF1	-7.94	1.09E-22	2.62E-19	-0.59	-10.59	4q23-q25
21	225619_at	FLJ30046	-4.32	1.33E-18	1.43E-15	-0.64	-10.58	13q21.33
22	204174_at	ALOX5AP	-3.76	2.38E-18	2.45E-15	-0.64	-10.57	13q12
23	202759_s_at	AKAP2	-3.59	5.54E-14	1.26E-11	-0.72	-10.50	9q31-q33
24	227429_at	MGC45840	-2.46	1.48E-15	6.02E-13	-0.68	-10.43	11p15.5
25	202954_at	UBE2C	-2.27	8.59E-15	2.73E-12	-0.69	-10.41	20q13.11

26	211984_at		-1.94	3.95E-14	9.48E-12	-0.71	-10.40	
27	243819_at		-2.71	9.01E-15	2.82E-12	-0.69	-10.38	
28	200700_s_at	KDELR2	-2.26	6.06E-13	1.06E-10	-0.75	-10.36	7p22.2
29	213292_s_at	SNX13	-1.82	1.39E-11	1.64E-09	-0.81	-10.26	7p21.1
30	228252_at	PIF1	-2.22	1.36E-12	2.14E-10	-0.75	-10.25	15q22.1
31	210140_at	CST7	-3.36	5.64E-18	5.07E-15	-0.61	-10.22	20p11.21
32	223609_at	ASP	-2.70	4.72E-18	4.43E-15	-0.61	-10.22	2p11.2
33	202022_at	ALDOC	-2.46	1.70E-14	4.64E-12	-0.67	-10.15	17cen-q12
34	214084_x_at	NCF1	-4.30	3.48E-20	6.27E-17	-0.57	-10.10	7q11.23
35	243134_at		-2.26	7.64E-14	1.67E-11	-0.66	-9.90	
36	207100_s_at	VAMP1	-2.75	1.44E-11	1.69E-09	-0.75	-9.86	12p
37	240093_x_at		-5.29	4.55E-20	7.56E-17	-0.55	-9.84	
38	219588_s_at	FLJ20311	-2.34	1.49E-13	3.09E-11	-0.66	-9.83	7q36.3
39	218865_at	FLJ22390	-6.91	5.25E-20	8.09E-17	-0.54	-9.81	1q42.11
40	206440_at	LIN7A	-5.59	6.36E-16	2.99E-13	-0.60	-9.75	12q21
41	235495_at	MGC20255	-2.67	4.04E-18	3.97E-15	-0.57	-9.75	19q13.13
42	202760_s_at	AKAP2	-4.76	4.88E-14	1.13E-11	-0.64	-9.72	9q31-q33
43	240027_at		-4.59	8.38E-19	9.52E-16	-0.55	-9.68	
44	211213_at	ORC5L	-4.64	6.37E-19	7.64E-16	-0.55	-9.67	7q22.1
45	227165_at	C13orf3	-1.83	2.73E-12	3.82E-10	-0.69	-9.66	13q11
46	229116_at		-5.89	1.74E-19	2.51E-16	-0.54	-9.64	
47	205716_at	MCFP	-2.24	4.17E-15	1.50E-12	-0.60	-9.64	7q21.12
48	221340_at	CDX4	-2.64	2.34E-16	1.37E-13	-0.58	-9.64	Xq13.2
49	230480_at	HIWI2	-2.75	5.45E-17	4.06E-14	-0.57	-9.60	11q21
50	208795_s_at	MCM7	-2.13	8.49E-13	1.42E-10	-0.66	-9.59	7q21.3-q22.1
1.8	AML_komplext versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	223318_s_at	MGC10974	-2.61	6.85E-20	1.15E-15	-0.73	-11.50	19p13.3
2	227056_at		-2.15	4.13E-16	1.39E-12	-0.76	-10.79	
3	222229_x_at		-1.38	8.42E-13	7.88E-10	-0.93	-10.20	
4	235502_at	PPP2CA	-2.66	8.78E-18	3.69E-14	-0.62	-10.05	5q23-q31
5	208645_s_at	RPS14	-1.31	9.83E-13	8.67E-10	-0.88	-10.01	5q31-q33
6	226694_at	AKAP2	-3.43	2.06E-19	1.74E-15	-0.57	-9.89	9q31-q33
7	244166_at		-3.44	4.34E-18	2.44E-14	-0.57	-9.68	
8	200608_s_at	RAD21	1.55	6.51E-12	3.37E-09	0.85	9.45	8q24
9	218600_at	MGC10986	-1.99	6.48E-14	9.88E-11	-0.62	-9.20	17q24.1
10	217729_s_at	AES	-1.92	2.92E-15	7.03E-12	-0.57	-9.17	19p13.3
11	231840_x_at	LOC90624	-1.91	7.04E-14	9.88E-11	-0.61	-9.07	5q31.1
12	200620_at	C1orf8	1.54	6.14E-11	2.23E-08	0.85	8.90	1p36-p31
13	208646_at	RPS14	-1.98	4.42E-12	2.66E-09	-0.68	-8.89	5q31-q33
14	203079_s_at	CUL2	1.99	8.73E-11	2.88E-08	0.87	8.84	10p11.21
15	202659_at	PSMB10	-2.16	1.10E-11	5.02E-09	-0.66	-8.62	16q22.1

16	225763_at	MGC21854	-2.03	4.09E-13	4.43E-10	-0.56	-8.57	1q22-q24
17	201807_at	VPS26	1.71	2.04E-10	6.04E-08	0.84	8.56	10q21.1
18	209190_s_at	DIAPH1	-1.69	1.80E-12	1.32E-09	-0.57	-8.42	5q31
19	211746_x_at	PSMA1	1.46	3.20E-10	8.68E-08	0.82	8.40	11p15.1
20	224368_s_at	NDRG3	-1.91	1.67E-11	7.04E-09	-0.62	-8.38	20q11.21-q11.23
21	206398_s_at	CD19	-4.51	2.86E-15	7.03E-12	-0.47	-8.36	16p11.2
22	213514_s_at	DIAPH1	-1.84	1.03E-12	8.67E-10	-0.54	-8.29	5q31
23	201920_at	SLC20A1	1.95	6.19E-10	1.41E-07	0.83	8.23	2q11-q14
24	224481_s_at	HECTD1	1.51	5.66E-10	1.32E-07	0.77	8.14	14q12
25	201676_x_at	PSMA1	1.47	6.89E-10	1.51E-07	0.79	8.14	11p15.1
26	209523_at	TAF2	1.97	1.25E-09	2.50E-07	0.85	8.07	8q24.12
27	201377_at	NICE-4	1.72	7.84E-10	1.69E-07	0.77	8.06	1q21.3
28	224875_at		-1.80	2.16E-12	1.46E-09	-0.51	-8.01	
29	222983_s_at	PAIP2	-1.45	2.29E-10	6.53E-08	-0.65	-8.01	5q31.3
30	221969_at	PAX5	-5.22	2.95E-14	6.21E-11	-0.44	-7.96	9p13
31	201263_at	TARS	1.87	1.47E-09	2.76E-07	0.78	7.91	5p13.2
32	201699_at	PSMC6	1.68	1.64E-09	2.94E-07	0.79	7.89	14q22.1
33	228737_at	C20orf100	-7.15	4.68E-14	8.74E-11	-0.44	-7.89	20q13.11
34	228664_at		-2.37	4.48E-13	4.43E-10	-0.47	-7.89	
35	222902_s_at	FLJ21144	1.57	6.41E-10	1.44E-07	0.68	7.88	1p34.1
36	213622_at	COL9A2	-2.13	1.63E-13	1.96E-10	-0.45	-7.87	1p33-p32
37	226781_at		-4.09	5.49E-14	9.25E-11	-0.44	-7.87	
38	212491_s_at	DNAJC8	1.49	1.49E-09	2.76E-07	0.76	7.86	1p35.2
39	212397_at	RDX	2.17	2.65E-09	4.37E-07	0.84	7.83	11q23
40	225635_s_at		-1.92	4.34E-13	4.43E-10	-0.46	-7.83	
41	201994_at	MORF4L2	1.41	1.29E-09	2.56E-07	0.71	7.78	Xq22
42	227203_at		-1.79	7.62E-11	2.62E-08	-0.55	-7.76	
43	214700_x_at	DKFZP434D193	2.21	3.74E-09	5.73E-07	0.86	7.76	2q23.3
44	201792_at	AEBP1	-3.92	1.18E-13	1.53E-10	-0.43	-7.75	7p13
45	202413_s_at	USP1	1.56	7.97E-10	1.70E-07	0.64	7.72	1p32.1-p31.3
46	225223_at		-1.88	2.77E-11	1.11E-08	-0.51	-7.70	
47	201548_s_at	PLU-1	1.70	1.78E-09	3.15E-07	0.67	7.62	1q32.1
48	228788_at	PPIL2	-2.36	1.64E-12	1.26E-09	-0.45	-7.62	22q11.21
49	208872_s_at	DP1	-1.83	6.99E-11	2.45E-08	-0.51	-7.59	5q22-q23
50	212058_at	SR140	1.55	5.02E-09	7.35E-07	0.80	7.59	3q23
1.9	AML_t(15;17) versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	204425_at	ARHGAP4	-18.20	9.73E-84	1.46E-79	-1.51	-27.05	Xq28
2	209732_at	CLECSF2	-26.43	1.38E-79	1.03E-75	-1.43	-25.70	12p13-p12
3	211990_at	HLA-DPA1	-9.05	7.33E-58	3.66E-54	-1.34	-23.26	6p21.3
4	205771_s_at	AKAP7	-8.69	8.46E-53	2.53E-49	-1.32	-22.67	6q23

5	213587_s_at	LOC155066	-6.05	6.13E-57	2.30E-53	-1.10	-19.73	7q36.1
6	227353_at	EVER2	-4.23	2.89E-26	2.47E-24	-1.31	-19.28	17q25.3
7	238949_at	FLJ31951	-9.28	3.35E-46	3.14E-43	-1.09	-18.90	5q33.3
8	201753_s_at	ADD3	-6.13	6.89E-37	2.29E-34	-1.14	-18.85	10q24.2-q24.3
9	226077_at	FLJ31951	-6.11	5.44E-39	2.91E-36	-1.11	-18.66	5q33.3
10	201923_at	PRDX4	-5.58	5.55E-33	1.03E-30	-1.15	-18.51	Xp22.13
11	201137_s_at	HLA-DPB1	-9.44	1.98E-51	4.94E-48	-1.03	-18.44	6p21.3
12	232617_at	CTSS	-5.47	2.85E-49	6.10E-46	-1.02	-18.13	1q21
13	236322_at		-7.03	4.86E-37	1.73E-34	-1.07	-17.99	
14	213106_at		-6.62	1.18E-42	8.07E-40	-1.03	-17.88	
15	227598_at	LOC113763	-5.31	1.40E-45	1.17E-42	-1.01	-17.84	7q35
16	201534_s_at	UBL3	-4.67	2.32E-42	1.51E-39	-1.03	-17.82	13q12-q13
17	201034_at	ADD3	-4.85	5.27E-27	4.87E-25	-1.15	-17.71	10q24.2-q24.3
18	204362_at	SCAP2	-11.44	4.38E-46	3.86E-43	-1.00	-17.65	7p21-p15
19	201669_s_at	MARCKS	-35.36	1.65E-48	3.08E-45	-0.99	-17.62	6q22.2
20	207697_x_at	LILRB2	-11.15	3.06E-47	4.17E-44	-0.99	-17.60	19q13.4
21	201752_s_at	ADD3	-4.42	4.34E-34	9.41E-32	-1.06	-17.57	10q24.2-q24.3
22	226106_at	ZFP26	-4.23	1.54E-33	3.09E-31	-1.06	-17.49	11p15.3
23	225386_s_at	LOC92906	-23.92	3.00E-48	5.00E-45	-0.97	-17.41	2p22.2
24	211991_s_at	HLA-DPA1	-14.34	7.22E-48	1.08E-44	-0.97	-17.38	6p21.3
25	236554_x_at	EVER2	-3.68	5.25E-25	3.75E-23	-1.15	-17.25	17q25.3
26	205882_x_at	ADD3	-4.17	2.22E-31	3.17E-29	-1.06	-17.20	10q24.2-q24.3
27	204661_at	CDW52	-19.50	3.88E-47	4.84E-44	-0.95	-17.14	1p36
28	203948_s_at	MPO	3.37	1.17E-16	2.76E-15	1.47	17.11	17q23.1
29	202901_x_at	CTSS	-6.41	1.12E-44	8.42E-42	-0.96	-17.03	1q21
30	210146_x_at	LILRB2	-14.78	1.63E-46	1.75E-43	-0.95	-17.00	19q13.4
31	34210_at	CDW52	-25.10	1.06E-46	1.22E-43	-0.94	-16.99	1p36
32	229041_s_at		-26.16	2.90E-46	2.90E-43	-0.95	-16.98	
33	205382_s_at	DF	5.60	3.76E-14	6.09E-13	1.87	16.90	19p13.3
34	200931_s_at	VCL	-4.01	6.04E-34	1.29E-31	-1.01	-16.85	10q22.1-q23
35	228370_at	SNURF	-9.14	5.49E-40	3.16E-37	-0.97	-16.81	15q12
36	212953_x_at	CALR	3.75	3.41E-13	4.83E-12	2.39	16.77	19p13.3-p13.2
37	214450_at	CTSW	10.82	5.73E-13	7.84E-12	2.70	16.71	11q13.1
38	219593_at	PHT2	-24.20	5.21E-45	4.11E-42	-0.94	-16.68	11q12.1
39	204563_at	SELL	-6.14	1.67E-39	9.24E-37	-0.95	-16.50	1q23-q25
40	226117_at	T2BP	-3.55	9.63E-37	3.07E-34	-0.96	-16.46	4q25
41	201719_s_at	EPB41L2	-10.87	2.47E-44	1.76E-41	-0.91	-16.45	6q23
42	38487_at	STAB1	13.57	1.06E-12	1.38E-11	2.69	16.20	3p21.31
43	203535_at	S100A9	-7.49	1.93E-30	2.52E-28	-0.99	-16.18	1q21
44	221004_s_at	ITM2C	6.00	4.41E-13	6.14E-12	2.10	16.12	2q37
45	209448_at	HTATIP2	-5.63	5.56E-37	1.94E-34	-0.93	-16.06	11p15.1
46	217478_s_at	HLA-DMA	-5.54	1.02E-36	3.18E-34	-0.93	-16.01	6p21.3
47	225639_at	SCAP2	-9.95	1.15E-36	3.51E-34	-0.92	-15.98	7p21-p15
48	209606_at	PSCDBP	-4.82	1.75E-29	2.04E-27	-0.98	-15.97	2q11.2
49	208771_s_at	LTA4H	-3.03	6.08E-37	2.07E-34	-0.92	-15.96	12q22
50	223663_at	FLJ37970	-6.25	7.79E-22	3.58E-20	-1.09	-15.94	11q12.3

1.10	AML_t(8;21) versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	224764_at	ARHGAP10	-7.14	6.90E-47	1.49E-42	-0.96	-17.27	10
2	221581_s_at	WBSCR5	-6.35	3.33E-44	3.59E-40	-0.94	-16.74	7q11.23
3	201811_x_at	SH3BP5	-6.29	3.63E-42	2.61E-38	-0.94	-16.56	3p24.3
4	218236_s_at	PRKCN	-5.63	4.73E-34	1.70E-30	-0.89	-15.23	2p21
5	215087_at		-3.11	3.30E-35	1.52E-31	-0.85	-14.83	
6	220066_at	CARD15	-6.95	9.26E-34	2.85E-30	-0.82	-14.39	16p12-q21
7	203741_s_at	ADCY7	-4.13	2.45E-26	2.20E-23	-0.89	-14.36	16q12-q13
8	212828_at	SYNJ2	-3.04	1.57E-27	1.99E-24	-0.87	-14.34	6q25.3
9	211084_x_at	PRKCN	-4.49	7.08E-22	2.46E-19	-0.95	-14.17	2p21
10	208146_s_at	CPVL	-9.12	3.53E-35	1.52E-31	-0.78	-14.08	7p15-p14
11	238012_at		-2.54	5.42E-27	6.47E-24	-0.85	-13.99	
12	233849_s_at	ARHGAP5	-5.33	3.63E-29	6.00E-26	-0.80	-13.68	14q12
13	201850_at	CAPG	-4.26	7.07E-31	1.52E-27	-0.77	-13.52	2cen-q24
14	201810_s_at	SH3BP5	-4.21	3.42E-29	6.00E-26	-0.79	-13.51	3p24.3
15	201425_at	ALDH2	-6.80	2.07E-25	1.35E-22	-0.82	-13.49	12q24.2
16	212895_s_at	ABR	-2.97	8.06E-26	5.98E-23	-0.81	-13.41	17p13.3
17	225615_at	LOC126917	-4.25	6.69E-29	1.03E-25	-0.77	-13.32	1p36.13
18	217963_s_at	NGFRAP1	-14.13	1.91E-32	5.13E-29	-0.74	-13.30	Xq22.1
19	203521_s_at	ZFP318	-2.30	1.79E-31	4.29E-28	-0.74	-13.27	6pter-p12.1
20	204494_s_at	DKFZP434H132	-2.62	1.39E-26	1.57E-23	-0.78	-13.19	15q22.33
21	238790_at		-4.46	1.23E-21	4.01E-19	-0.83	-12.94	
22	204495_s_at	DKFZP434H132	-2.72	1.57E-28	2.25E-25	-0.74	-12.91	15q22.33
23	210612_s_at	SYNJ2	-6.96	2.80E-28	3.77E-25	-0.74	-12.86	6q25.3
24	213908_at		-5.60	1.77E-30	3.47E-27	-0.71	-12.83	
25	211962_s_at	ZFP36L1	-3.68	3.55E-22	1.36E-19	-0.79	-12.68	14q22-q24
26	225786_at	LOC284702	-3.39	1.85E-26	1.73E-23	-0.72	-12.48	1q44
27	38269_at	PRKD2	-2.25	1.02E-24	5.21E-22	-0.72	-12.23	19q13.2
28	218474_s_at	FLJ20040	-2.60	6.86E-19	1.33E-16	-0.81	-12.18	16p13.3
29	225227_at		-3.64	1.48E-26	1.59E-23	-0.69	-12.12	
30	211965_at	ZFP36L1	-3.73	2.58E-25	1.54E-22	-0.70	-12.05	14q22-q24
31	207124_s_at	GNB5	-6.61	6.03E-26	4.64E-23	-0.69	-12.02	15q15.3
32	204000_at	GNB5	-3.27	2.22E-25	1.39E-22	-0.68	-11.89	15q15.3
33	226206_at	FLJ32205	-2.11	9.03E-19	1.70E-16	-0.78	-11.85	7p22.3
34	203232_s_at	SCA1	-6.99	4.12E-25	2.28E-22	-0.68	-11.85	6p23
35	212423_at	FLJ90798	-3.30	2.71E-19	5.94E-17	-0.76	-11.84	10q22.3
36	218608_at	HSA9947	-5.77	7.54E-21	2.22E-18	-0.73	-11.79	1p36
37	203505_at	ABCA1	-5.91	1.66E-26	1.62E-23	-0.66	-11.75	9q31.1
38	226865_at		-3.93	3.42E-26	2.94E-23	-0.66	-11.74	
39	204057_at	ICSBP1	-3.98	1.58E-26	1.62E-23	-0.65	-11.70	16q24.1
40	226134_s_at		-4.14	5.28E-26	4.21E-23	-0.65	-11.67	

41	226673_at	SH2D3C	-4.13	1.71E-21	5.50E-19	-0.71	-11.65	9q34.12
42	208091_s_at	DKFZP564K0822	-10.61	4.11E-26	3.40E-23	-0.64	-11.58	7p14.1
43	202732_at	PKIG	-2.61	3.99E-25	2.26E-22	-0.65	-11.55	20q12-q13.1
44	207104_x_at	LILRB1	-5.88	2.26E-25	1.39E-22	-0.65	-11.54	19q13.4
45	221866_at	TFEB	-3.05	1.30E-23	5.81E-21	-0.67	-11.52	6p21
46	202887_s_at	RTP801	-3.16	2.03E-22	7.95E-20	-0.67	-11.43	10pter-q26.12
47	225240_s_at		-3.79	2.87E-25	1.67E-22	-0.64	-11.43	
48	207839_s_at	LOC51754	-2.63	5.78E-14	3.62E-12	-0.92	-11.42	9p13.1
49	230894_s_at		-5.79	8.42E-25	4.53E-22	-0.64	-11.42	
50	240572_s_at		-6.74	1.44E-25	1.03E-22	-0.63	-11.41	
1.11	CLL versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	202503_s_at	KIAA0101	-25.91	2.26E-106	3.53E-102	-1.97	-34.65	15q22.1
2	202589_at	TYMS	-30.97	1.83E-102	1.43E-98	-1.90	-33.46	18p11.32
3	226936_at		-10.02	8.08E-91	4.21E-87	-1.60	-28.76	
4	208864_s_at	TXN	-5.34	6.51E-69	4.24E-66	-1.69	-28.76	9q31
5	204798_at	MYB	-19.19	9.25E-90	3.61E-86	-1.58	-28.50	6q22-q23
6	203675_at	NUCB2	-24.32	4.98E-83	1.56E-79	-1.52	-27.06	11p15.1-p14
7	224838_at	FOXP1	4.85	3.06E-26	5.45E-25	2.85	26.63	3p14.1
8	218883_s_at	FLJ23468	-6.06	2.10E-82	5.47E-79	-1.47	-26.39	4q35.1
9	226546_at		-10.03	4.52E-80	1.01E-76	-1.47	-26.15	
10	207168_s_at	H2AFY	-2.84	1.66E-37	6.99E-36	-1.82	-26.06	5q31.3-q32
11	232232_s_at	CT2	-13.61	2.64E-79	5.16E-76	-1.42	-25.52	6q22.1
12	210613_s_at	SYNGR1	-21.84	1.57E-78	2.73E-75	-1.42	-25.43	22q13.1
13	219076_s_at	PXMP2	-5.82	5.57E-75	6.69E-72	-1.43	-25.39	12q24.33
14	201163_s_at	IGFBP7	-21.77	1.55E-76	2.20E-73	-1.40	-25.04	4q12
15	219869_s_at	BIGM103	-6.10	2.18E-77	3.41E-74	-1.39	-24.97	4q22-q24
16	211626_x_at	ERG	-7.75	1.80E-72	1.65E-69	-1.39	-24.79	21q22.3
17	228249_at	LOC119710	-7.34	7.52E-75	8.40E-72	-1.36	-24.52	11p12
18	202441_at	KEO4	-6.88	1.22E-75	1.58E-72	-1.36	-24.50	10q21-q22
19	213911_s_at	H2AFZ	-2.23	1.73E-45	1.33E-43	-1.55	-24.47	4q24
20	202580_x_at	FOXM1	-15.48	3.70E-73	3.62E-70	-1.35	-24.12	12p13
21	222036_s_at	MCM4	-5.94	1.16E-73	1.21E-70	-1.33	-23.97	8q12-q13
22	202338_at	TK1	-4.90	2.05E-69	1.45E-66	-1.33	-23.70	17q23.2-q25.3
23	212141_at	MCM4	-11.25	3.83E-72	3.32E-69	-1.32	-23.66	8q12-q13
24	210052_s_at	C20orf1	-11.05	1.10E-70	9.05E-68	-1.30	-23.30	20q11.2
25	222680_s_at	RAMP	-5.73	1.86E-70	1.45E-67	-1.30	-23.30	
26	211709_s_at	SCGF	-26.57	1.91E-68	1.10E-65	-1.33	-23.27	19q13.3
27	206111_at	RNASE2	-24.48	5.11E-70	3.80E-67	-1.30	-23.22	14q24-q31
28	228868_x_at	CDT1	-6.30	9.98E-69	6.24E-66	-1.29	-23.13	16q24.3
29	201231_s_at	ENO1	-3.30	5.55E-49	5.22E-47	-1.40	-23.02	1p36.3-p36.2
30	224428_s_at	CDCA7	-13.78	3.53E-69	2.40E-66	-1.28	-22.99	2q31
31	214501_s_at	H2AFY	-4.65	1.53E-56	2.75E-54	-1.33	-22.88	5q31.3-q32

32	201310_s_at	C5orf13	-16.96	1.07E-68	6.41E-66	-1.26	-22.74	5q22.1
33	201200_at	CREG	-5.23	2.53E-51	3.14E-49	-1.35	-22.65	1q24
34	213008_at	FLJ10719	-11.05	1.32E-67	7.39E-65	-1.24	-22.39	15q25-q26
35	200896_x_at	HDGF	-2.86	1.53E-50	1.69E-48	-1.33	-22.33	Xq25
36	AFFX-HUMGAPDH/M33197_3_at - HG-U133B	GAPD	-2.28	9.68E-30	2.34E-28	-1.68	-22.31	12p13
37	209267_s_at	BIGM103	-6.31	4.25E-67	2.21E-64	-1.24	-22.30	4q22-q24
38	228273_at		-9.83	2.72E-67	1.47E-64	-1.24	-22.29	
39	229838_at	NUCB2	-14.94	1.30E-66	6.55E-64	-1.24	-22.25	11p15.1-p14
40	202705_at	CCNB2	-12.73	5.05E-65	2.47E-62	-1.25	-22.14	15q21.2
41	210046_s_at	IDH2	-4.52	2.28E-64	9.88E-62	-1.23	-22.07	15q26.1
42	202487_s_at	H2AV	-2.78	7.25E-56	1.23E-53	-1.27	-21.93	7p13
43	225927_at		4.05	1.40E-23	2.00E-22	2.24	21.92	
44	204026_s_at	ZWINT	-6.40	8.17E-65	3.76E-62	-1.22	-21.89	10q21-q22
45	201829_at	NET1	-8.70	7.00E-65	3.32E-62	-1.21	-21.76	10p15
46	229307_at		-14.20	2.01E-64	8.97E-62	-1.21	-21.73	
47	224578_at	TD-60	-2.36	1.64E-50	1.80E-48	-1.28	-21.59	1p36.13
48	211714_x_at	OK/SW-cl.56	-3.96	4.58E-61	1.46E-58	-1.21	-21.55	6p21.31
49	232233_at	CT2	-4.02	1.10E-62	3.99E-60	-1.20	-21.45	6q22.1
50	203949_at	MPO	-93.51	1.21E-61	3.95E-59	-1.24	-21.42	17q23.1
1.12	CML versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	205557_at	BPI	6.20	2.63E-34	1.13E-31	1.97	24.77	20q11.23-q12
2	212531_at	LCN2	7.09	8.58E-33	2.86E-30	1.87	23.37	9q34
3	206676_at	CEACAM8	6.91	2.56E-32	7.79E-30	1.83	22.93	19q13.2
4	201029_s_at	CD99	-4.01	1.15E-68	2.04E-64	-1.26	-22.73	Xp22.32
5	210254_at	MS4A3	3.69	1.18E-34	5.48E-32	1.46	20.88	11q12
6	211657_at	CEACAM6	5.81	8.77E-30	1.64E-27	1.63	20.52	19q13.2
7	212268_at	SERPINB1	2.48	1.18E-36	7.72E-34	1.36	20.37	6p25
8	203757_s_at	CEACAM6	7.19	3.85E-28	5.49E-26	1.70	20.18	19q13.2
9	209771_x_at	CD24	3.56	7.72E-32	1.92E-29	1.40	19.57	6q21
10	207269_at	DEFA4	4.93	1.43E-29	2.57E-27	1.46	19.31	8p23
11	202018_s_at	LTF	3.89	1.48E-30	3.08E-28	1.40	19.19	3q21-q23
12	216379_x_at	KIAA1919	3.71	1.52E-30	3.12E-28	1.39	19.13	6q22
13	206871_at	ELA2	3.04	7.21E-36	4.10E-33	1.20	18.69	19p13.3
14	203021_at	SLPI	5.34	2.73E-27	3.44E-25	1.50	18.69	20q12
15	200858_s_at	RPS8	-1.42	4.80E-37	3.53E-34	-1.18	-18.68	1p34.1-p32
16	210244_at	CAMP	11.41	4.66E-25	4.11E-23	1.71	18.48	3p21.3
17	207802_at	SGP28	16.56	1.44E-24	1.19E-22	1.80	18.48	6p12.3
18	205513_at	TCN1	6.33	4.06E-26	4.24E-24	1.51	18.20	11q11-q12
19	201061_s_at	STOM	3.31	3.22E-28	4.66E-26	1.37	18.19	9q34.1
20	223423_at	GPCR1	4.04	5.53E-26	5.67E-24	1.49	18.03	3q26.2-q27

21	211275_s_at	GYG	2.95	1.84E-27	2.43E-25	1.38	18.02	3q24-q25.1
22	205863_at	S100A12	4.51	2.78E-26	2.98E-24	1.45	17.94	1q21
23	203936_s_at	MMP9	9.25	5.78E-24	4.27E-22	1.73	17.87	20q11.2-q13.1
24	201554_x_at	GYG	3.38	2.69E-27	3.42E-25	1.36	17.78	3q24-q25.1
25	205653_at	CTSG	4.71	2.41E-26	2.63E-24	1.38	17.59	14q11.2
26	225958_at	M6PR	-1.94	1.20E-40	2.12E-37	-1.03	-17.46	12p13
27	225386_s_at	LOC92906	3.53	6.92E-28	9.32E-26	1.28	17.46	2p22.2
28	208700_s_at	TKT	2.44	7.51E-27	8.77E-25	1.33	17.43	3p14.3
29	213503_x_at	ANXA2	-3.61	2.90E-48	2.56E-44	-0.96	-17.39	15q21-q22
30	219281_at	MSRA	3.07	4.43E-24	3.36E-22	1.55	17.35	8p23.1
31	221952_x_at	KIAA1393	1.84	1.03E-26	1.18E-24	1.32	17.31	14q23.1
32	204174_at	ALOX5AP	3.92	2.96E-25	2.72E-23	1.41	17.29	13q12
33	213572_s_at	SERPINB1	2.17	8.70E-30	1.64E-27	1.17	17.15	6p25
34	201590_x_at	ANXA2	-3.39	4.56E-47	2.68E-43	-0.95	-17.09	15q21-q22
35	202332_at	CSNK1E	-2.78	3.77E-42	1.11E-38	-0.98	-16.99	22q13.1
36	214575_s_at	AZU1	3.89	7.79E-27	9.04E-25	1.24	16.82	19p13.3
37	205786_s_at	ITGAM	4.05	2.81E-24	2.24E-22	1.38	16.70	16p11.2
38	204351_at	S100P	3.65	2.82E-25	2.61E-23	1.30	16.67	4p16
39	208308_s_at	GPI	2.47	1.88E-26	2.10E-24	1.23	16.64	19q13.1
40	209772_s_at	CD24	6.72	1.58E-23	1.07E-21	1.45	16.63	6q21
41	208699_x_at	TKT	2.71	5.78E-25	4.97E-23	1.29	16.51	3p14.3
42	208650_s_at	CD24	4.58	3.75E-24	2.90E-22	1.33	16.37	6q21
43	231688_at		5.26	4.44E-24	3.36E-22	1.33	16.32	
44	210427_x_at	ANXA2	-3.28	6.56E-44	2.89E-40	-0.91	-16.31	15q21-q22
45	212414_s_at	SEPT6	-3.01	2.06E-43	7.26E-40	-0.90	-16.22	Xq24
46	200654_at	P4HB	1.99	6.47E-32	1.63E-29	1.03	16.22	17q25
47	209369_at	ANXA3	7.49	2.22E-22	1.25E-20	1.48	16.11	4q13-q22
48	204670_x_at	HLA-DRB5	-3.73	6.06E-42	1.53E-38	-0.90	-16.06	6p21.3
49	206851_at	RNASE3	4.56	4.62E-23	2.93E-21	1.33	15.87	14q24-q31
50	266_s_at	CD24	4.21	1.88E-23	1.26E-21	1.28	15.83	6q21
1.13	normalBM versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	204285_s_at	PMAIP1	-6.31	1.56E-33	1.36E-29	-1.16	-19.31	18q21.31
2	204286_s_at	PMAIP1	-9.67	1.96E-44	3.40E-40	-0.95	-16.96	18q21.31
3	208690_s_at	PDLIM1	-3.65	1.76E-25	2.04E-22	-0.96	-15.80	10q22-q26.3
4	209806_at	HIST1H2BK	-2.86	7.39E-20	3.21E-17	-1.01	-15.67	6p21.33
5	224767_at		-4.72	2.78E-24	2.32E-21	-0.95	-15.57	
6	217988_at	HEI10	-2.28	1.52E-16	3.89E-14	-1.03	-15.24	14q11.1
7	201595_s_at	HT010	-1.73	2.11E-16	5.31E-14	-1.03	-15.23	2q32.1
8	208549_x_at	LOC51685	-2.10	8.24E-14	1.33E-11	-1.08	-15.00	14
9	210281_s_at	ZNF198	-2.92	5.24E-15	1.05E-12	-1.03	-14.88	13q11-q12
10	238389_s_at		-3.25	1.32E-14	2.38E-12	-0.97	-14.12	

11	210396_s_at		-2.05	1.91E-14	3.35E-12	-0.98	-14.10	
12	200631_s_at	SET	-1.59	2.03E-10	1.53E-08	-1.14	-13.94	9q34
13	40189_at	SET	-1.68	3.15E-11	2.94E-09	-1.08	-13.93	9q34
14	36711_at	MAFF	-6.93	7.05E-28	1.11E-24	-0.81	-13.90	22q13.1
15	202722_s_at	GFPT1	-1.67	9.68E-18	3.12E-15	-0.89	-13.83	2p13
16	214455_at	HIST1H2BC	-7.59	6.41E-24	5.06E-21	-0.83	-13.81	6p21.3
17	242832_at	PER1	-8.79	5.00E-30	1.45E-26	-0.78	-13.71	17p13.1-17p12
18	212099_at		-3.38	1.01E-26	1.46E-23	-0.80	-13.64	
19	202018_s_at	LTF	3.03	2.20E-08	9.51E-07	1.37	13.56	3q21-q23
20	208754_s_at	NAP1L1	-2.09	3.81E-13	5.06E-11	-0.96	-13.54	12q21.1
21	215111_s_at	TSC22	-3.87	1.40E-30	5.66E-27	-0.77	-13.50	13q14
22	201830_s_at	NET1	-3.38	1.44E-28	2.78E-25	-0.77	-13.36	10p15
23	201015_s_at	JUP	-10.37	1.63E-30	5.66E-27	-0.75	-13.25	17q21
24	226608_at	SAS10	-2.32	5.03E-15	1.03E-12	-0.88	-13.20	4q13.3
25	204900_x_at	SAP30	-3.87	2.80E-24	2.32E-21	-0.78	-13.17	4q34.1
26	222067_x_at	HIST1H2BD	-3.92	1.25E-29	3.09E-26	-0.74	-13.12	6p21.3
27	201416_at	SOX4	-4.96	3.25E-31	1.88E-27	-0.72	-13.03	6p22.3
28	204011_at	SPRY2	-5.43	1.61E-24	1.47E-21	-0.76	-13.01	13q22.1
29	201417_at		-3.15	2.06E-23	1.56E-20	-0.76	-12.89	
30	212241_at	GRINL1A	-1.75	6.17E-12	6.54E-10	-0.94	-12.84	15q22.1
31	224763_at	MAPK8IP2	-2.24	1.04E-22	7.25E-20	-0.76	-12.80	22q13.33
32	218224_at	PNMA1	-2.58	1.38E-22	9.24E-20	-0.76	-12.75	14q24.1
33	238333_s_at	LOC92170	-3.32	6.53E-25	6.31E-22	-0.74	-12.71	10q26.3
34	218247_s_at	LOC51320	-2.94	8.59E-14	1.37E-11	-0.86	-12.68	18q21.1
35	204805_s_at	TGM2	-2.83	2.07E-10	1.56E-08	-0.99	-12.67	20q12
36	209398_at	HIST1H1C	-5.05	5.30E-29	1.15E-25	-0.71	-12.61	6p21.3
37	232322_x_at	STARD10	-3.45	3.06E-26	3.80E-23	-0.72	-12.60	11q13
38	208546_x_at	HIST1H2BH	-4.13	2.97E-15	6.37E-13	-0.83	-12.60	6p21.3
39	230894_s_at		-7.50	6.00E-28	1.04E-24	-0.71	-12.52	
40	215411_s_at	C6orf4	-2.68	6.95E-13	8.82E-11	-0.87	-12.44	6q21
41	207121_s_at	MAPK6	-1.96	8.17E-17	2.29E-14	-0.79	-12.44	15q21
42	201917_s_at	FLJ10618	-2.67	4.14E-09	2.26E-07	-1.07	-12.41	3q23
43	221517_s_at	CRSP6	-3.14	2.15E-12	2.49E-10	-0.88	-12.40	11q14
44	234875_at		-1.61	4.57E-11	4.08E-09	-0.93	-12.39	
45	212420_at	ELF1	-2.48	3.25E-11	3.02E-09	-0.92	-12.37	13q13
46	222594_s_at	FLJ13117	-4.38	1.59E-26	2.12E-23	-0.70	-12.31	12q13.12
47	222669_s_at	SBDS	-2.30	3.39E-13	4.60E-11	-0.84	-12.26	7q11.21
48	236193_at	HIST1H2BC	-5.21	2.44E-16	6.06E-14	-0.78	-12.22	6p21.3
49	217722_s_at	NEUGRIN	-1.82	2.86E-21	1.65E-18	-0.72	-12.14	15q26.1
50	204203_at	CEBPG	-2.10	6.92E-11	5.81E-09	-0.91	-12.13	19q13.11

Table 2
2. All-Pairs (AP)

2.1	ALL_MLL versus ALL_Ph+							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	204069_at	MEIS1	40.29	5.62E-09	1.88E-05	2.62	11.17	2p14-p13
2	225637_at	FLJ20186	-5.19	1.98E-11	6.45E-07	-1.66	-10.17	16q24.3
3	225563_at	LOC255967	3.83	3.77E-09	1.61E-05	1.88	10.11	13q12.13
4	201874_at	MPZL1	2.42	1.23E-09	9.99E-06	1.79	10.11	1q23.2
5	34210_at	CDW52	-12.07	6.62E-10	7.19E-06	-1.74	-9.75	1p36
6	227353_at	EVER2	-3.59	2.04E-10	3.32E-06	-1.61	-9.61	17q25.3
7	219463_at	C20orf103	38.91	3.65E-08	5.66E-05	2.00	9.54	20p12
8	205055_at	ITGAE	2.37	1.76E-09	1.08E-05	1.64	9.49	17p13
9	242414_at		5.63	4.41E-08	6.38E-05	1.90	9.31	
10	204661_at	CDW52	-12.08	3.94E-09	1.61E-05	-1.62	-8.97	1p36
11	219033_at	FLJ21308	3.85	3.18E-08	5.45E-05	1.57	8.64	5q11.1
12	223046_at	EGLN1	-5.85	5.78E-09	1.88E-05	-1.52	-8.64	1q42.1
13	221969_at	PAX5	3.91	5.91E-08	7.70E-05	1.61	8.58	9p13
14	231887_s_at	KIAA1274	-3.44	1.99E-09	1.08E-05	-1.41	-8.50	10q22.1
15	233500_x_at	LLT1	7.57	1.20E-07	1.13E-04	1.65	8.44	12p13
16	200871_s_at	PSAP	-3.70	1.12E-08	2.61E-05	-1.43	-8.25	10q21-q22
17	208146_s_at	CPVL	-5.60	1.22E-08	2.66E-05	-1.35	-7.97	7p15-p14
18	230643_at		-5.24	8.72E-09	2.23E-05	-1.32	-7.94	
19	209822_s_at	VLDLR	9.55	4.67E-07	2.46E-04	1.63	7.90	9p24
20	228083_at	CACNA2D4	9.51	1.75E-07	1.50E-04	1.44	7.85	12p13.33
21	202853_s_at	RYK	-4.11	1.32E-08	2.68E-05	-1.29	-7.78	3q22
22	238021_s_at		5.82	2.18E-07	1.69E-04	1.43	7.76	
23	239214_at		5.58	3.74E-07	2.20E-04	1.47	7.69	
24	204328_at	EVER1	-2.28	7.40E-09	2.19E-05	-1.22	-7.60	17q25.3
25	227584_at		-3.91	1.87E-08	3.57E-05	-1.24	-7.53	
26	225703_at	KIAA1545	2.14	4.69E-08	6.38E-05	1.26	7.53	12q24.33
27	218966_at	MYO5C	-4.31	1.19E-07	1.13E-04	-1.37	-7.48	15q21
28	224252_s_at	FXYD5	-1.83	8.90E-09	2.23E-05	-1.19	-7.44	19q12-q13.1
29	225912_at	TP53INP1	-9.01	1.44E-07	1.27E-04	-1.37	-7.42	8q22
30	243756_at		2.99	6.31E-08	7.81E-05	1.22	7.35	
31	238022_at		4.46	3.45E-07	2.11E-04	1.32	7.34	
32	201105_at	LGALS1	6.98	3.78E-07	2.20E-04	1.31	7.30	22q13.1
33	204044_at	QPRT	6.09	1.55E-06	5.00E-04	1.53	7.25	16p12.1
34	217967_s_at	C1orf24	-3.77	7.57E-08	8.51E-05	-1.22	-7.24	1q25
35	200953_s_at	CCND2	-7.08	3.07E-07	1.96E-04	-1.38	-7.17	12p13
36	228046_at	LOC152485	-4.47	6.47E-08	7.81E-05	-1.19	-7.16	4q31.1
37	222868_s_at	IL18BP	-2.33	1.09E-07	1.11E-04	-1.21	-7.14	11q13
38	224772_at	NAV1	-4.63	1.26E-07	1.14E-04	-1.23	-7.14	
39	201875_s_at	FLJ21047	1.98	3.06E-08	5.45E-05	1.14	7.13	1q23.2
40	221497_x_at	EGLN1	-4.07	1.02E-07	1.07E-04	-1.19	-7.09	1q42.1

Table 2.1-2.78

41	209170_s_at	GPM6B	12.86	2.25E-06	6.47E-04	1.51	7.07	Xp22.2
42	215925_s_at	CD72	6.14	1.06E-06	4.06E-04	1.31	7.03	9p13.1
43	219686_at	HSA250839	-20.05	4.36E-07	2.45E-04	-1.36	-7.02	4p16.2
44	242172_at		8.83	2.56E-06	6.89E-04	1.52	7.02	
45	214022_s_at	MGC27165	-4.60	2.08E-07	1.69E-04	-1.22	-7.01	14
46	206099_at	PRKCH	-2.92	8.45E-08	9.17E-05	-1.15	-6.99	14q22-q23
47	202052_s_at	RAI14	-9.02	2.98E-07	1.96E-04	-1.24	-6.97	5p13.3-p13.2
48	229390_at		-3.38	4.70E-08	6.38E-05	-1.11	-6.94	
49	243618_s_at	LOC152485	-13.40	5.38E-07	2.73E-04	-1.33	-6.91	4q31.1
50	205672_at	XPA	-2.67	3.58E-08	5.66E-05	-1.09	-6.88	9q22.3
2.2	ALL_MLL versus ALL_T-lineage							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	213539_at	CD3D	-31.00	1.82E-12	3.82E-08	-2.63	-13.77	11q23
2	226496_at	FLJ22611	14.40	1.35E-10	6.46E-07	2.77	13.62	9p12
3	225314_at	MGC45416	-7.94	5.21E-12	4.36E-08	-2.32	-12.70	4p11
4	221969_at	PAX5	28.36	2.90E-09	3.24E-06	2.56	11.58	9p13
5	231902_at	LOC152485	-3.59	3.71E-12	4.14E-08	-1.78	-10.87	4q31.1
6	204069_at	MEIS1	20.91	6.05E-09	5.47E-06	2.27	10.80	2p14-p13
7	202789_at		-4.91	2.28E-12	3.82E-08	-1.74	-10.75	
8	226878_at		4.57	1.54E-09	2.14E-06	1.97	10.63	
9	244876_at		4.11	6.86E-10	1.35E-06	1.89	10.60	
10	228046_at	LOC152485	-13.63	2.82E-10	9.53E-07	-1.95	-10.50	4q31.1
11	226764_at	LOC152485	-40.14	5.60E-10	1.17E-06	-2.13	-10.42	4q31.1
12	225563_at	LOC255967	3.91	3.16E-09	3.35E-06	1.88	10.16	13q12.13
13	226459_at	FLJ35564	9.08	1.61E-08	1.02E-05	2.06	10.02	10q23.33
14	212827_at	IGHM	8.78	7.57E-09	6.29E-06	1.81	9.73	14q32.33
15	219463_at	C20orf103	47.99	4.07E-08	1.97E-05	2.18	9.66	20p12
16	222895_s_at	BCL11B	-18.24	1.05E-09	1.67E-06	-1.75	-9.66	14q32.31
17	217800_s_at	NDFIP1	-8.14	8.87E-10	1.48E-06	-1.68	-9.54	5q31.3
18	209619_at	CD74	5.84	3.85E-10	9.53E-07	1.58	9.51	5q32
19	201029_s_at	CD99	-2.02	2.02E-11	1.35E-07	-1.48	-9.37	Xp22.32
20	225703_at	KIAA1545	2.80	1.39E-09	2.02E-06	1.58	9.31	12q24.33
21	219033_at	FLJ21308	4.97	8.32E-09	6.47E-06	1.67	9.28	5q11.1
22	222422_s_at	NDFIP1	-5.31	5.36E-11	2.99E-07	-1.48	-9.26	5q31.3
23	239214_at		21.85	6.68E-08	2.79E-05	1.96	9.19	
24	217478_s_at	HLA-DMA	6.60	2.87E-08	1.67E-05	1.76	9.18	6p21.3
25	201720_s_at	LAPTM5	3.09	3.49E-10	9.53E-07	1.50	9.18	1p34
26	228007_at		-5.15	3.99E-10	9.53E-07	-1.52	-9.18	
27	233500_x_at	LLT1	13.73	6.23E-08	2.71E-05	1.92	9.17	12p13
28	244189_at		-2.57	4.96E-10	1.11E-06	-1.53	-9.16	
29	204949_at	ICAM3	-5.90	1.96E-09	2.52E-06	-1.60	-9.13	19p13.3-p13.2
30	208788_at	HELO1	-3.24	3.86E-10	9.53E-07	-1.50	-9.10	6p21.1-p12.1
31	218205_s_at	MKNK2	3.26	2.72E-08	1.62E-05	1.72	9.09	19p13.3

Table 2.1-2.78

32	211990_at	HLA-DPA1	5.15	2.17E-09	2.69E-06	1.51	8.98	6p21.3
33	214172_x_at	RYK	-3.93	8.55E-10	1.48E-06	-1.49	-8.93	3q22
34	225637_at	FLJ20186	-4.42	2.92E-10	9.53E-07	-1.44	-8.92	16q24.3
35	209374_s_at	IGHM	9.33	2.94E-08	1.67E-05	1.65	8.89	14q32.33
36	217979_at	NET-6	5.71	1.13E-08	8.02E-06	1.57	8.89	7p21.1
37	227353_at	EVER2	-4.33	3.30E-09	3.35E-06	-1.55	-8.86	17q25.3
38	207697_x_at	LILRB2	5.39	8.94E-09	6.80E-06	1.54	8.83	19q13.4
39	227247_at		-3.82	1.34E-09	2.02E-06	-1.48	-8.81	
40	205689_at	KIAA0435	-5.41	2.10E-10	8.78E-07	-1.41	-8.81	1q42.2
41	243756_at		4.17	5.86E-09	5.45E-06	1.50	8.76	
42	215925_s_at	CD72	69.67	1.93E-07	5.71E-05	2.03	8.66	9p13.1
43	206804_at	CD3G	-26.40	1.48E-08	9.88E-06	-1.70	-8.64	11q23
44	209536_s_at	EHD4	3.82	4.72E-08	2.16E-05	1.60	8.62	15q11.1
45	218764_at	PRKCH	-5.38	2.38E-09	2.74E-06	-1.44	-8.59	14q22-q23
46	218942_at	FLJ22055	-5.52	1.65E-09	2.21E-06	-1.41	-8.52	12q13.13
47	224710_at	RAB34	5.30	3.28E-09	3.35E-06	1.41	8.50	17q11.1
48	241871_at		-12.12	1.62E-08	1.02E-05	-1.57	-8.45	
49	202853_s_at	RYK	-5.98	8.11E-09	6.46E-06	-1.48	-8.44	3q22
50	244261_at	IL28RA	20.36	2.00E-07	5.79E-05	1.75	8.42	1p36.11
2.3	ALL_MLL versus ALL_t(8;14)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	225563_at	LOC255967	8.73	6.43E-10	2.51E-06	2.76	12.61	13q12.13
2	204798_at	MYB	7.19	8.01E-11	9.21E-07	2.42	12.36	6q22-q23
3	203373_at	SOCS2	34.53	1.89E-09	3.78E-06	2.66	11.88	12q
4	215537_x_at	DDAH2	9.01	4.55E-10	2.23E-06	2.30	11.56	6p21.3
5	212207_at	KIAA1025	4.99	1.12E-10	9.21E-07	2.21	11.52	12q24.22
6	204069_at	MEIS1	25.72	6.19E-09	1.01E-05	2.47	10.97	2p14-p13
7	212481_s_at	TPM4	4.25	2.13E-09	3.78E-06	2.20	10.84	19p13.1
8	214909_s_at	DDAH2	6.07	1.77E-09	3.78E-06	2.16	10.78	6p21.3
9	226496_at	FLJ22611	5.39	1.41E-10	9.21E-07	2.00	10.69	9p12
10	242414_at		11.83	9.79E-09	1.25E-05	2.23	10.38	
11	204446_s_at	ALOX5	-9.94	1.52E-07	6.31E-05	-2.33	-10.15	10q11.2
12	224710_at	RAB34	8.55	1.65E-09	3.78E-06	1.94	10.08	17q11.1
13	201417_at		5.18	1.99E-09	3.78E-06	1.89	9.84	
14	214623_at	FBXW3	6.32	8.93E-10	2.91E-06	1.84	9.79	22q11
15	202853_s_at	RYK	-4.14	1.40E-08	1.44E-05	-1.86	-9.51	3q22
16	225314_at	MGC45416	-4.42	1.90E-07	7.01E-05	-2.05	-9.45	4p11
17	201015_s_at	JUP	12.01	1.09E-08	1.25E-05	1.85	9.39	17q21
18	217168_s_at	HERPUD1	-3.41	1.98E-08	1.84E-05	-1.83	-9.36	16q12.2-q13
19	219033_at	FLJ21308	4.85	1.24E-08	1.35E-05	1.85	9.35	5q11.1
20	202262_x_at	DDAH2	6.26	9.29E-09	1.25E-05	1.82	9.31	6p21.3
21	217979_at	NET-6	6.04	1.52E-08	1.48E-05	1.84	9.26	7p21.1
22	211671_s_at	NR3C1	5.47	7.11E-08	3.97E-05	1.93	9.02	5q31

Table 2.1-2.78

23	223276_at	NID67	8.58	2.52E-08	2.14E-05	1.76	8.93	5q33.1
24	238750_at		7.48	4.85E-08	3.49E-05	1.80	8.86	
25	228083_at	CACNA2D4	19.61	1.53E-07	6.31E-05	1.99	8.76	12p13.33
26	204759_at	CHC1L	4.46	1.08E-08	1.25E-05	1.64	8.69	13q14.3
27	202887_s_at	RTP801	4.51	5.72E-08	3.50E-05	1.73	8.64	10pter-q26.12
28	231982_at		27.52	1.75E-07	6.57E-05	1.92	8.62	
29	201540_at	FHL1	10.02	1.58E-07	6.32E-05	1.83	8.54	Xq26
30	213792_s_at	INSR	12.42	1.55E-07	6.31E-05	1.81	8.51	19p13.3-p13.2
31	221581_s_at	WBSCR5	5.53	7.81E-08	4.12E-05	1.71	8.50	7q11.23
32	212208_at	KIAA1025	4.42	7.34E-08	3.98E-05	1.68	8.44	12q24.22
33	201416_at	SOX4	6.00	2.82E-08	2.30E-05	1.62	8.43	6p22.3
34	203796_s_at	BCL7A	3.98	5.77E-08	3.50E-05	1.66	8.43	12q24.13
35	224681_at	GNA12	6.23	1.31E-07	5.69E-05	1.69	8.31	7p22-p21
36	203372_s_at	SOCS2	48.70	3.33E-07	1.10E-04	1.94	8.30	12q
37	226668_at	FLJ36175	3.85	5.00E-08	3.49E-05	1.57	8.18	2q24.2
38	201865_x_at	NR3C1	4.48	1.97E-07	7.14E-05	1.66	8.11	5q31
39	225592_at	NRM	2.57	5.33E-08	3.50E-05	1.54	8.06	6p21.31
40	209267_s_at	BIGM103	5.79	2.66E-07	9.12E-05	1.68	8.06	4q22-q24
41	226043_at	AGS3	5.84	1.12E-07	5.62E-05	1.58	8.05	9q34.3
42	212509_s_at		15.08	4.62E-07	1.33E-04	1.81	8.04	
43	239214_at		6.87	2.21E-07	7.70E-05	1.64	8.03	
44	226528_at		-4.18	7.47E-07	1.87E-04	-1.67	-8.02	
45	209822_s_at	VLDLR	10.39	4.48E-07	1.31E-04	1.78	8.02	9p24
46	205055_at	ITGAE	2.35	1.01E-08	1.25E-05	1.46	8.01	17p13
47	204044_at	QPRT	12.88	4.33E-07	1.31E-04	1.76	8.01	16p12.1
48	202481_at	SDR1	5.94	5.80E-08	3.50E-05	1.53	8.00	1p36.1
49	220987_s_at	SNARK	-2.88	3.88E-07	1.24E-04	-1.59	-7.95	1q32.1
50	209112_at	CDKN1B	2.57	4.93E-08	3.49E-05	1.47	7.82	12p13.1-p12
2.4	ALL_MLL versus AML_MLL							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	211404_s_at	APLP2	-5.96	6.57E-19	1.69E-14	-2.16	-15.05	11q24
2	208702_x_at	APLP2	-8.08	2.12E-16	1.95E-12	-2.22	-14.46	11q24
3	214875_x_at	APLP2	-7.65	5.77E-15	2.41E-11	-2.10	-13.30	11q24
4	200742_s_at	CLN2	-4.08	2.28E-16	1.95E-12	-1.85	-12.86	11p15
5	201858_s_at	PRG1	-2.96	1.90E-14	6.10E-11	-1.75	-12.01	10q22.1
6	217800_s_at	NDFIP1	-11.20	5.64E-14	1.61E-10	-1.84	-12.00	5q31.3
7	204122_at	TYROBP	-9.13	9.55E-14	2.04E-10	-1.87	-11.97	19q13.1
8	41220_at	MSF	2.81	1.96E-11	8.54E-09	1.93	11.95	17q25
9	226496_at	FLJ22611	7.75	2.98E-11	1.09E-08	1.90	11.73	9p12
10	225703_at	KIAA1545	3.89	4.55E-10	9.83E-08	2.10	11.69	12q24.33
11	225775_at		3.93	6.11E-12	3.74E-09	1.80	11.60	
12	206111_at	RNASE2	-5.21	1.85E-15	1.19E-11	-1.63	-11.55	14q24-q31
13	244876_at		4.68	9.76E-10	1.78E-07	2.13	11.48	

Table 2.1-2.78

14	221969_at	PAX5	22.69	3.24E-09	4.54E-07	2.47	11.47	9p13
15	200743_s_at	CLN2	-2.86	6.58E-15	2.41E-11	-1.61	-11.36	11p15
16	212207_at	KIAA1025	3.98	9.91E-10	1.78E-07	2.08	11.35	12q24.22
17	219013_at	GALNT11	-6.74	1.33E-13	2.45E-10	-1.68	-11.27	7q34-q36
18	227853_at		-5.79	6.43E-15	2.41E-11	-1.59	-11.23	
19	223120_at	MGC1314	-3.91	7.16E-14	1.67E-10	-1.64	-11.20	6q24
20	205639_at	AOAH	-21.77	8.63E-13	9.23E-10	-1.80	-11.19	7p14-p12
21	229215_at	ASCL2	-9.01	3.50E-13	5.00E-10	-1.66	-11.02	11p15.5
22	213116_at	NEK3	-5.48	1.86E-13	3.18E-10	-1.62	-10.96	13q14.13
23	203799_at	BIMLEC	-5.01	2.27E-13	3.44E-10	-1.58	-10.76	2q24.2
24	222422_s_at	NDFIP1	-9.98	5.33E-13	6.85E-10	-1.59	-10.70	5q31.3
25	214181_x_at	LST1	-7.23	1.30E-12	1.24E-09	-1.63	-10.66	6p21.3
26	230015_at		9.33	6.50E-09	7.52E-07	2.10	10.61	
27	210314_x_at	TNFSF13	-6.33	1.19E-13	2.34E-10	-1.52	-10.60	17p13.1
28	211581_x_at	LST1	-5.45	4.96E-13	6.71E-10	-1.56	-10.60	6p21.3
29	225563_at	LOC255967	4.40	1.81E-09	2.93E-07	1.87	10.59	13q12.13
30	209500_x_at	TNFSF13	-5.42	5.69E-13	6.96E-10	-1.55	-10.52	17p13.1
31	211474_s_at	SERPINB6	-5.31	9.80E-13	9.68E-10	-1.56	-10.49	6p25
32	200975_at	PPT1	-3.28	7.16E-14	1.67E-10	-1.49	-10.47	1p32
33	217979_at	NET-6	10.43	8.86E-09	9.81E-07	2.07	10.42	7p21.1
34	218942_at	FLJ22055	-6.32	2.24E-13	3.44E-10	-1.50	-10.41	12q13.13
35	211582_x_at	LST1	-6.14	1.45E-12	1.28E-09	-1.56	-10.40	6p21.3
36	200871_s_at	PSAP	-5.81	4.34E-12	2.86E-09	-1.60	-10.32	10q21-q22
37	202788_at	MAPKAPK3	-2.80	7.60E-13	8.48E-10	-1.51	-10.30	3p21.3
38	215633_x_at	LST1	-6.86	5.11E-12	3.28E-09	-1.59	-10.26	6p21.3
39	243756_at		5.45	6.16E-09	7.27E-07	1.89	10.22	
40	214574_x_at	LST1	-5.95	3.56E-12	2.54E-09	-1.55	-10.19	6p21.3
41	210629_x_at	LST1	-4.83	2.78E-12	2.16E-09	-1.50	-10.07	6p21.3
42	235033_at		-3.62	1.76E-12	1.50E-09	-1.48	-10.07	
43	223168_at	ARHU	-8.52	1.23E-11	6.08E-09	-1.58	-10.01	1q42.11-q42.3
44	222764_at	ASRGL1	-13.69	1.06E-11	5.50E-09	-1.55	-9.99	11q12.2
45	216041_x_at	GRN	-7.60	6.60E-12	3.85E-09	-1.51	-9.98	17q21.32
46	204971_at	CSTA	-6.40	2.95E-12	2.18E-09	-1.46	-9.92	3q21
47	203796_s_at	BCL7A	6.49	1.68E-08	1.63E-06	1.95	9.92	12q24.13
48	202382_s_at	GNPI	-13.15	1.28E-11	6.21E-09	-1.54	-9.90	5q21
49	203041_s_at	LAMP2	-4.02	2.35E-12	1.89E-09	-1.45	-9.89	Xq24
50	200661_at	PPGB	-6.06	4.07E-12	2.75E-09	-1.46	-9.86	20q13.1
2.5	ALL_MLL versus AML_inv(16)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	203949_at	MPO	-16.62	1.02E-25	2.78E-21	-4.54	-28.75	17q23.1
2	203948_s_at	MPO	-27.99	1.12E-18	7.64E-15	-3.97	-22.74	17q23.1
3	203973_s_at	CEBPD	-15.58	1.92E-17	8.71E-14	-3.22	-19.06	8p11.2-p11.1
4	203585_at	ZNF185	-5.46	3.42E-19	3.11E-15	-2.92	-18.38	Xq28

Table 2.1-2.78

5	208702_x_at	APLP2	-6.85	1.54E-16	5.99E-13	-2.78	-16.83	11q24
6	200953_s_at	CCND2	-7.78	1.62E-15	4.03E-12	-2.88	-16.66	12p13
7	208248_x_at	APLP2	-5.07	3.26E-19	3.11E-15	-2.56	-16.51	11q24
8	225789_at	CENTG3	-6.00	5.47E-18	2.98E-14	-2.51	-16.01	7q36.1
9	204949_at	ICAM3	-8.53	1.08E-15	2.95E-12	-2.67	-15.99	19p13.3-p13.2
10	224918_x_at	MGST1	-41.86	1.10E-13	1.11E-10	-2.84	-14.90	12p12.3-p12.1
11	204661_at	CDW52	-17.50	2.69E-14	3.19E-11	-2.53	-14.71	1p36
12	231310_at		-7.69	1.14E-14	1.94E-11	-2.38	-14.35	
13	205382_s_at	DF	-21.30	2.28E-14	2.83E-11	-2.37	-14.19	19p13.3
14	200951_s_at	CCND2	-19.84	3.59E-13	2.88E-10	-2.59	-13.98	12p13
15	226496_at	FLJ22611	16.06	1.68E-10	3.52E-08	2.95	13.85	9p12
16	200665_s_at	SPARC	-10.29	2.78E-13	2.45E-10	-2.46	-13.81	5q31.3-q32
17	34210_at	CDW52	-16.29	1.46E-13	1.38E-10	-2.34	-13.65	1p36
18	231736_x_at	MGST1	-33.49	1.22E-12	7.10E-10	-2.55	-13.34	12p12.3-p12.1
19	200661_at	PPGB	-5.09	6.64E-16	2.26E-12	-2.07	-13.32	20q13.1
20	204214_s_at	RAB32	-5.51	1.38E-14	2.09E-11	-2.12	-13.22	6q24.2
21	228058_at	LOC124220	-16.46	6.53E-13	4.21E-10	-2.34	-13.22	16p13.3
22	201012_at	ANXA1	-3.30	7.47E-16	2.27E-12	-2.04	-13.19	9q12-q21.2
23	214875_x_at	APLP2	-7.18	8.07E-13	5.01E-10	-2.32	-13.10	11q24
24	201605_x_at	CNN2	-2.56	4.75E-14	5.40E-11	-2.09	-13.08	21q11.1
25	211404_s_at	APLP2	-5.52	1.57E-14	2.26E-11	-2.09	-13.07	11q24
26	204563_at	SELL	-9.20	6.05E-13	4.07E-10	-2.24	-12.97	1q23-q25
27	223120_at	MGC1314	-3.25	4.49E-15	1.02E-11	-1.99	-12.74	6q24
28	204122_at	TYROBP	-9.86	1.51E-12	8.26E-10	-2.26	-12.73	19q13.1
29	38487_at	STAB1	-5.69	2.17E-14	2.82E-11	-2.02	-12.71	3p21.31
30	208704_x_at	APLP2	-4.72	9.68E-15	1.76E-11	-2.00	-12.69	11q24
31	224391_s_at	CSE-C	-4.15	2.34E-13	2.13E-10	-2.09	-12.65	11q24
32	224583_at	COTL1	-6.46	5.37E-13	3.75E-10	-2.10	-12.53	16q23.3
33	233177_s_at	MR-1	-2.65	8.00E-15	1.68E-11	-1.95	-12.49	2q35
34	229776_at	SLC21A11	-3.97	4.55E-13	3.34E-10	-2.00	-12.37	15q26
35	208683_at	CAPN2	-6.62	9.90E-14	1.04E-10	-1.98	-12.32	1q41-q42
36	217849_s_at	CDC42BPB	-19.24	4.67E-12	1.99E-09	-2.23	-12.28	14q32.3
37	224252_s_at	FXYD5	-2.41	8.65E-15	1.69E-11	-1.89	-12.18	19q12-q13.1
38	225602_at	C9orf19	-4.46	3.45E-13	2.85E-10	-1.98	-12.15	9p13-p12
39	201360_at	CST3	-47.02	9.47E-12	3.69E-09	-2.37	-12.15	20p11.21
40	200871_s_at	PSAP	-5.68	2.51E-12	1.24E-09	-2.07	-12.06	10q21-q22
41	217967_s_at	C1orf24	-7.19	2.54E-12	1.24E-09	-2.03	-11.93	1q25
42	225563_at	LOC255967	6.31	1.13E-09	1.60E-07	2.41	11.91	13q12.13
43	225510_at		-7.02	4.28E-13	3.30E-10	-1.92	-11.85	
44	217989_at	RetSDR2	-2.51	1.31E-14	2.09E-11	-1.83	-11.84	4q21.3
45	203373_at	SOCS2	27.97	2.02E-09	2.51E-07	2.53	11.78	12q
46	200975_at	PPT1	-2.91	2.01E-14	2.74E-11	-1.82	-11.76	1p32
47	208891_at	DUSP6	-5.31	1.24E-13	1.21E-10	-1.86	-11.75	12q22-q23
48	221059_s_at	CHST6	-5.45	3.03E-12	1.45E-09	-1.98	-11.72	16q22
49	215706_x_at	ZYX	-3.63	5.65E-14	6.17E-11	-1.82	-11.65	7q32
50	221969_at	PAX5	30.98	3.01E-09	3.44E-07	2.68	11.65	9p13

Table 2.1-2.78

2.6	ALL_MLL versus AML_inv(3)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	204949_at	ICAM3	-8.93	1.24E-10	1.20E-06	-2.52	-12.69	19p13.3-p13.2
2	226496_at	FLJ22611	7.58	9.89E-11	1.20E-06	2.28	12.14	9p12
3	221969_at	PAX5	22.08	3.48E-09	4.28E-06	2.59	11.47	9p13
4	210024_s_at	UBE2E3	-9.74	6.65E-10	2.19E-06	-2.16	-11.16	2q32.1
5	244876_at		4.15	1.83E-09	3.78E-06	2.22	11.11	
6	227353_at	EVER2	-4.65	6.76E-10	2.19E-06	-2.07	-10.90	17q25.3
7	225563_at	LOC255967	4.55	2.41E-09	4.25E-06	2.16	10.88	13q12.13
8	204214_s_at	RAB32	-3.49	2.09E-11	6.31E-07	-1.77	-10.35	6q24.2
9	202888_s_at	ANPEP	-7.88	3.17E-09	4.28E-06	-1.93	-10.06	15q25-q26
10	219033_at	FLJ21308	5.51	1.02E-08	8.09E-06	1.94	9.83	5q11.1
11	219463_at	C20orf103	143.42	3.52E-08	1.71E-05	2.36	9.82	20p12
12	217963_s_at	NGFRAP1	-31.63	1.87E-08	1.15E-05	-2.17	-9.81	Xq22.1
13	228058_at	LOC124220	-7.63	3.69E-09	4.28E-06	-1.85	-9.81	16p13.3
14	203725_at	GADD45A	-3.72	5.62E-10	2.19E-06	-1.72	-9.72	1p31.2-p31.1
15	218942_at	FLJ22055	-6.70	1.88E-09	3.78E-06	-1.78	-9.71	12q13.13
16	221752_at	SSH1	-2.81	2.56E-10	1.54E-06	-1.69	-9.69	12q24.12
17	225799_at	MGC4677	-5.22	3.38E-09	4.28E-06	-1.80	-9.67	2p11.1
18	222422_s_at	NDFIP1	-6.31	7.25E-10	2.19E-06	-1.70	-9.58	5q31.3
19	201462_at	KIAA0193	-12.42	2.20E-08	1.27E-05	-2.01	-9.55	7p14.3-p14.1
20	242414_at		6.69	2.33E-08	1.32E-05	1.94	9.55	
21	213716_s_at	SECTM1	-5.49	3.36E-09	4.28E-06	-1.76	-9.54	17q25
22	201494_at	PRCP	-2.66	2.61E-09	4.25E-06	-1.73	-9.49	11q14
23	60471_at	RIN3	-3.71	1.59E-10	1.20E-06	-1.62	-9.48	14q32.13
24	243756_at		5.16	2.68E-09	4.25E-06	1.72	9.48	
25	201200_at	CREG	-2.79	3.09E-10	1.55E-06	-1.64	-9.48	1q24
26	223136_at	AIG-1	-7.89	1.15E-08	8.54E-06	-1.80	-9.36	6q24.1
27	233500_x_at	LLT1	15.40	6.10E-08	2.40E-05	2.04	9.30	12p13
28	211581_x_at	LST1	-4.32	3.96E-09	4.42E-06	-1.68	-9.24	6p21.3
29	214574_x_at	LST1	-4.55	9.33E-09	7.61E-06	-1.72	-9.19	6p21.3
30	224910_at		2.78	1.69E-08	1.11E-05	1.75	9.18	
31	230292_at		3.87	2.11E-08	1.25E-05	1.76	9.14	
32	239214_at		17.95	8.48E-08	2.88E-05	2.05	9.14	
33	219457_s_at	RIN3	-5.12	3.31E-09	4.28E-06	-1.64	-9.12	14q32.13
34	203796_s_at	BCL7A	5.08	1.83E-08	1.15E-05	1.71	9.05	12q24.13
35	215051_x_at	AIF1	-3.74	2.34E-09	4.25E-06	-1.60	-9.03	6p21.3
36	203373_at	SOCS2	5.06	7.21E-09	6.80E-06	1.64	9.00	12q
37	200953_s_at	CCND2	-5.89	4.70E-08	2.17E-05	-1.85	-8.98	12p13
38	211582_x_at	LST1	-4.43	9.19E-09	7.61E-06	-1.64	-8.92	6p21.3
39	200951_s_at	CCND2	-14.09	7.37E-08	2.73E-05	-1.93	-8.89	12p13
40	201243_s_at	ATP1B1	-13.89	7.41E-08	2.73E-05	-1.92	-8.87	1q22-q25
41	217800_s_at	NDFIP1	-11.26	6.03E-08	2.40E-05	-1.82	-8.84	5q31.3

42	200602_at	APP	-15.46	8.23E-08	2.88E-05	-1.87	-8.77	21q21.3
43	214181_x_at	LST1	-5.80	4.13E-08	1.98E-05	-1.70	-8.73	6p21.3
44	244261_at	IL28RA	36.41	1.77E-07	4.89E-05	2.02	8.70	1p36.11
45	225592_at	NRM	2.63	6.93E-08	2.64E-05	1.71	8.66	6p21.31
46	201829_at	NET1	-3.62	2.53E-08	1.39E-05	-1.60	-8.59	10p15
47	215925_s_at	CD72	45.33	2.13E-07	5.47E-05	2.00	8.59	9p13.1
48	218818_at	FHL3	-2.20	9.56E-10	2.62E-06	-1.46	-8.58	1p34
49	225314_at	MGC45416	-4.69	6.16E-08	2.40E-05	-1.69	-8.57	4p11
50	215633_x_at	LST1	-4.80	5.47E-08	2.29E-05	-1.66	-8.54	6p21.3
2.7	ALL_MLL versus AML_komplext							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	226496_at	FLJ22611	12.38	1.42E-10	4.01E-08	2.58	13.41	9p12
2	202788_at	MAPKAPK3	-2.62	1.05E-15	2.08E-11	-1.69	-11.93	3p21.3
3	204852_s_at	PTPN7	-4.33	7.05E-15	4.65E-11	-1.70	-11.81	1q32.1
4	202853_s_at	RYK	-5.62	5.68E-15	4.65E-11	-1.67	-11.69	3q22
5	200871_s_at	PSAP	-5.54	1.09E-13	2.39E-10	-1.73	-11.49	10q21-q22
6	221969_at	PAX5	22.70	3.20E-09	3.37E-07	2.45	11.46	9p13
7	203373_at	SOCS2	11.61	3.68E-09	3.62E-07	2.22	11.09	12q
8	201200_at	CREG	-2.86	1.99E-14	9.84E-11	-1.50	-10.71	1q24
9	200975_at	PPT1	-3.48	4.84E-14	1.60E-10	-1.49	-10.60	1p32
10	227353_at	EVER2	-4.12	3.12E-13	6.16E-10	-1.54	-10.59	17q25.3
11	215051_x_at	AIF1	-3.63	4.64E-14	1.60E-10	-1.47	-10.46	6p21.3
12	217967_s_at	C1orf24	-11.05	3.56E-12	3.52E-09	-1.65	-10.44	1q25
13	214172_x_at	RYK	-3.68	8.78E-14	2.17E-10	-1.47	-10.40	3q22
14	200620_at	C1orf8	-1.93	6.11E-14	1.73E-10	-1.45	-10.36	1p36-p31
15	210024_s_at	UBE2E3	-8.50	4.10E-12	3.65E-09	-1.48	-9.94	2q32.1
16	225563_at	LOC255967	3.91	1.93E-09	2.35E-07	1.66	9.93	13q12.13
17	213095_x_at	AIF1	-4.10	8.71E-13	1.44E-09	-1.42	-9.92	6p21.3
18	204949_at	ICAM3	-9.71	1.28E-11	7.18E-09	-1.55	-9.89	19p13.3-p13.2
19	225613_at	KIAA0303	-5.43	2.14E-12	2.35E-09	-1.43	-9.88	5q12.3
20	219615_s_at	KCNK5	-3.25	1.03E-11	6.81E-09	-1.48	-9.77	6p21
21	208864_s_at	TXN	-2.29	1.24E-12	1.75E-09	-1.39	-9.75	9q31
22	203139_at	DAPK1	-7.50	1.17E-11	7.06E-09	-1.47	-9.71	9q34.1
23	225782_at	LOC253827	-30.69	3.07E-11	1.38E-08	-1.58	-9.70	12q14.1
24	219463_at	C20orf103	53.28	3.93E-08	2.08E-06	2.14	9.68	20p12
25	207654_x_at	DR1	-2.28	6.56E-13	1.18E-09	-1.36	-9.67	1p22.1
26	218942_at	FLJ22055	-8.10	6.90E-12	4.87E-09	-1.42	-9.67	12q13.13
27	225789_at	CENTG3	-5.25	3.93E-12	3.65E-09	-1.40	-9.66	7q36.1
28	202381_at	ADAM9	-7.23	4.50E-12	3.71E-09	-1.40	-9.66	8p11.21
29	217800_s_at	NDFIP1	-8.26	1.15E-11	7.06E-09	-1.45	-9.66	5q31.3
30	209188_x_at	DR1	-2.33	1.44E-12	1.89E-09	-1.36	-9.61	1p22.1
31	201201_at	CSTB	-3.93	9.96E-13	1.51E-09	-1.35	-9.60	21q22.3
32	203796_s_at	BCL7A	5.24	2.90E-08	1.67E-06	1.80	9.43	12q24.13

Table 2.1-2.78

33	235033_at		-2.57	1.60E-12	1.97E-09	-1.32	-9.41	
34	204328_at	EVER1	-2.63	2.00E-12	2.33E-09	-1.32	-9.40	17q25.3
35	203725_at	GADD45A	-5.24	1.79E-11	9.32E-09	-1.39	-9.39	1p31.2-p31.1
36	209804_at	DCLRE1A	-6.74	5.90E-12	4.32E-09	-1.34	-9.38	10q25.1
37	218168_s_at	CABC1	-2.78	2.26E-12	2.36E-09	-1.32	-9.37	1q42.13
38	209340_at	UAP1	-2.86	4.24E-12	3.65E-09	-1.32	-9.33	1q23.1
39	239214_at		23.92	6.77E-08	3.06E-06	1.99	9.26	
40	232543_x_at	ARHGAP9	-3.36	3.22E-11	1.38E-08	-1.38	-9.23	12q14
41	218910_at	FLJ10375	-8.54	6.45E-11	2.28E-08	-1.40	-9.16	3p21.32
42	225790_at	LOC253827	-25.47	1.44E-10	4.01E-08	-1.48	-9.10	12q14.1
43	216652_s_at		-2.26	5.44E-12	4.14E-09	-1.28	-9.09	
44	201012_at	ANXA1	-2.98	4.78E-12	3.78E-09	-1.27	-9.06	9q12-q21.2
45	227481_at	FLJ31349	-5.41	3.14E-11	1.38E-08	-1.32	-9.05	6q25.2
46	217963_s_at	NGFRAP1	-26.34	1.68E-10	4.50E-08	-1.47	-9.04	Xq22.1
47	208891_at	DUSP6	-4.61	1.31E-11	7.18E-09	-1.29	-9.03	12q22-q23
48	244741_s_at		-8.46	9.58E-11	3.05E-08	-1.38	-9.02	
49	203973_s_at	CEBPD	-8.76	7.34E-11	2.46E-08	-1.36	-9.02	8p11.2-p11.1
50	209901_x_at	AIF1	-4.78	2.73E-11	1.28E-08	-1.30	-8.98	6p21.3
2.8	ALL_MLL versus AML_t(15;17)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	203949_at	MPO	-21.90	2.92E-20	6.32E-16	-5.21	-29.25	17q23.1
2	203948_s_at	MPO	-50.34	9.06E-17	3.27E-13	-5.30	-26.30	17q23.1
3	224918_x_at	MGST1	-76.09	1.51E-15	4.07E-12	-5.01	-23.47	12p12.3-p12.1
4	231736_x_at	MGST1	-63.73	1.33E-14	2.06E-11	-4.47	-20.87	12p12.3-p12.1
5	206871_at	ELA2	-14.24	6.78E-17	3.10E-13	-3.65	-20.60	19p13.3
6	205382_s_at	DF	-45.39	4.08E-15	9.81E-12	-3.97	-20.54	19p13.3
7	200654_at	P4HB	-4.60	5.91E-19	6.39E-15	-3.43	-20.35	17q25
8	212953_x_at	CALR	-5.70	8.58E-15	1.55E-11	-3.39	-18.36	19p13.3-p13.2
9	214450_at	CTSW	-18.36	1.32E-13	1.43E-10	-3.32	-17.18	11q13.1
10	38487_at	STAB1	-45.09	4.47E-13	4.20E-10	-3.63	-17.14	3p21.31
11	208689_s_at	RPN2	-3.32	1.08E-17	7.78E-14	-2.67	-16.19	20q12-q13.1
12	214575_s_at	AZU1	-29.25	9.85E-13	7.75E-10	-3.22	-16.01	19p13.3
13	221739_at	IL27w	-2.49	7.17E-17	3.10E-13	-2.64	-15.86	19p13.3
14	200953_s_at	CCND2	-11.41	2.59E-12	1.81E-09	-3.06	-15.18	12p13
15	205624_at	CPA3	-94.78	5.09E-12	3.34E-09	-3.29	-15.05	3q21-q25
16	221004_s_at	ITM2C	-6.12	9.69E-15	1.61E-11	-2.47	-14.53	2q37
17	206111_at	RNASE2	-5.26	5.18E-16	1.60E-12	-2.33	-14.14	14q24-q31
18	210788_s_at	retSDR4	-3.66	1.00E-12	7.75E-10	-2.54	-14.01	14q22.3
19	226496_at	FLJ22611	18.36	1.43E-10	5.03E-08	2.99	13.95	9p12
20	208675_s_at	DDOST	-3.42	5.20E-15	1.06E-11	-2.23	-13.47	1p36.1
21	201012_at	ANXA1	-3.29	5.40E-15	1.06E-11	-2.15	-13.08	9q12-q21.2
22	217716_s_at	SEC61A1	-2.79	1.86E-14	2.68E-11	-2.17	-13.04	3q21.3
23	200951_s_at	CCND2	-27.01	7.18E-11	2.88E-08	-2.71	-12.85	12p13

Table 2.1-2.78

24	218910_at	FLJ10375	-12.12	3.53E-11	1.82E-08	-2.45	-12.72	3p21.32
25	233072_at	KIAA1857	-16.57	6.50E-11	2.79E-08	-2.56	-12.69	9q34
26	203591_s_at	CSF3R	-13.93	6.40E-11	2.79E-08	-2.53	-12.64	1p35-p34.3
27	208852_s_at	CANX	-3.44	4.06E-13	3.99E-10	-2.13	-12.52	5q35
28	210024_s_at	UBE2E3	-4.90	2.50E-14	3.38E-11	-2.04	-12.40	2q32.1
29	201494_at	PRCP	-4.27	3.05E-11	1.61E-08	-2.31	-12.37	11q14
30	201360_at	CST3	-37.70	1.80E-10	5.91E-08	-2.65	-12.24	20p11.21
31	208612_at	GRP58	-2.55	6.35E-14	7.81E-11	-2.01	-12.20	15q15
32	201666_at	TIMP1	-7.00	8.72E-12	5.55E-09	-2.16	-12.17	Xp11.3-p11.23
33	200068_s_at - HG-U133B	CANX	-1.98	6.50E-14	7.81E-11	-2.00	-12.14	5q35
34	204150_at	STAB1	-51.98	2.57E-10	7.45E-08	-2.59	-11.98	3p21.31
35	218084_x_at	FXYD5	-2.39	1.29E-13	1.43E-10	-1.97	-11.93	19q12-q13.1
36	221969_at	PAX5	67.66	2.38E-09	4.40E-07	2.81	11.87	9p13
37	226878_at		6.53	9.29E-10	2.12E-07	2.40	11.87	
38	204347_at	AK3	-11.28	2.31E-12	1.67E-09	-2.03	-11.85	1p31.3
39	203373_at	SOCS2	26.52	2.15E-09	4.20E-07	2.58	11.77	12q
40	201596_x_at	KRT18	-26.67	3.37E-10	9.34E-08	-2.48	-11.74	12q13
41	200663_at	CD63	-2.83	1.42E-13	1.47E-10	-1.93	-11.70	12q12-q13
42	225563_at	LOC255967	5.97	1.02E-09	2.27E-07	2.33	11.67	13q12.13
43	214315_x_at	CALR	-3.37	1.55E-11	9.29E-09	-2.05	-11.65	19p13.3-p13.2
44	205663_at	PCBP3	-3.96	6.59E-11	2.79E-08	-2.09	-11.48	21q22.3
45	225790_at	LOC253827	-37.66	5.83E-10	1.50E-07	-2.40	-11.37	12q14.1
46	41220_at	MSF	2.59	5.72E-11	2.63E-08	1.99	11.30	17q25
47	200986_at	SERPING1	-25.55	7.33E-10	1.78E-07	-2.44	-11.26	11q12-q13.1
48	200656_s_at	P4HB	-7.49	3.78E-10	1.02E-07	-2.18	-11.22	17q25
49	204069_at	MEIS1	45.29	5.38E-09	8.15E-07	2.62	11.21	2p14-p13
50	238365_s_at		-5.93	2.58E-10	7.45E-08	-2.12	-11.19	
2.9	ALL_MLL versus AML_t(8;21)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	203949_at	MPO	-20.09	2.74E-18	7.56E-14	-3.49	-20.62	17q23.1
2	203948_s_at	MPO	-36.79	3.12E-14	2.86E-10	-2.89	-15.59	17q23.1
3	202853_s_at	RYK	-4.88	3.51E-16	4.83E-12	-2.11	-13.56	3q22
4	226496_at	FLJ22611	9.79	2.84E-10	1.82E-07	2.74	13.21	9p12
5	228058_at	LOC124220	-19.36	1.41E-12	3.00E-09	-2.33	-12.93	16p13.3
6	202788_at	MAPKAPK3	-4.21	5.45E-13	2.14E-09	-2.18	-12.79	3p21.3
7	200953_s_at	CCND2	-4.13	1.84E-13	1.02E-09	-2.03	-12.44	12p13
8	225563_at	LOC255967	6.64	9.91E-10	4.71E-07	2.44	12.02	13q12.13
9	224918_x_at	MGST1	-39.17	1.66E-11	2.70E-08	-2.27	-11.80	12p12.3-p12.1
10	204852_s_at	PTPN7	-4.25	8.91E-13	2.49E-09	-1.89	-11.61	1q32.1
11	202382_s_at	GNPI	-14.60	9.69E-12	1.78E-08	-2.01	-11.53	5q21
12	217800_s_at	NDFIP1	-6.66	8.31E-13	2.49E-09	-1.86	-11.53	5q31.3
13	238790_at		7.07	2.62E-10	1.72E-07	2.00	11.28	

Table 2.1-2.78

14	221969_at	PAX5	14.73	4.88E-09	1.24E-06	2.49	11.20	9p13
15	204069_at	MEIS1	43.24	5.48E-09	1.35E-06	2.62	11.19	2p14-p13
16	244876_at		4.32	9.70E-10	4.71E-07	2.04	11.07	
17	210024_s_at	UBE2E3	-6.20	9.93E-13	2.49E-09	-1.75	-11.03	2q32.1
18	208248_x_at	APLP2	-3.68	1.82E-13	1.02E-09	-1.69	-10.93	11q24
19	208864_s_at	TXN	-2.37	1.29E-12	2.96E-09	-1.72	-10.86	9q31
20	203373_at	SOCS2	10.36	2.99E-09	8.32E-07	2.09	10.81	12q
21	41220_at	MSF	2.41	1.25E-10	1.04E-07	1.81	10.74	17q25
22	225703_at	KIAA1545	3.31	6.95E-10	3.61E-07	1.90	10.69	12q24.33
23	211474_s_at	SERPINB6	-6.60	4.73E-11	5.51E-08	-1.82	-10.60	6p25
24	212207_at	KIAA1025	3.52	1.13E-09	5.02E-07	1.90	10.59	12q24.22
25	209318_x_at	PLAGL1	-5.51	6.00E-12	1.18E-08	-1.70	-10.58	6q24-q25
26	206871_at	ELA2	-12.06	5.60E-11	5.51E-08	-1.83	-10.57	19p13.3
27	231736_x_at	MGST1	-30.18	1.73E-10	1.22E-07	-2.02	-10.51	12p12.3-p12.1
28	217989_at	RetSDR2	-2.36	5.37E-13	2.14E-09	-1.61	-10.46	4q21.3
29	214172_x_at	RYK	-3.30	9.41E-13	2.49E-09	-1.61	-10.38	3q22
30	212827_at	IGHM	11.25	1.02E-08	2.01E-06	2.12	10.35	14q32.33
31	203796_s_at	BCL7A	8.32	9.82E-09	1.96E-06	2.10	10.33	12q24.13
32	225637_at	FLJ20186	-7.39	5.07E-11	5.51E-08	-1.71	-10.25	16q24.3
33	224910_at		3.52	2.23E-09	6.82E-07	1.83	10.19	
34	208702_x_at	APLP2	-4.58	4.82E-11	5.51E-08	-1.68	-10.15	11q24
35	221581_s_at	WBSCR5	15.98	2.08E-08	3.32E-06	2.22	10.09	7q11.23
36	202887_s_at	RTP801	8.21	1.62E-08	2.84E-06	2.07	10.05	10pter-q26.12
37	228827_at		-85.32	4.66E-10	2.68E-07	-1.98	-10.02	
38	203973_s_at	CEBPD	-8.39	1.31E-10	1.06E-07	-1.66	-9.89	8p11.2-p11.1
39	211728_s_at	HYAL3	-6.94	1.47E-10	1.10E-07	-1.65	-9.83	3p21.3
40	200871_s_at	PSAP	-3.23	3.45E-11	4.57E-08	-1.57	-9.79	10q21-q22
41	219463_at	C20orf103	91.29	3.70E-08	5.23E-06	2.31	9.78	20p12
42	227353_at	EVER2	-3.53	5.60E-11	5.51E-08	-1.57	-9.73	17q25.3
43	235703_at		-4.27	3.48E-11	4.57E-08	-1.55	-9.72	
44	218486_at		-24.07	9.26E-10	4.64E-07	-1.84	-9.64	
45	228894_at		-5.24	2.12E-10	1.43E-07	-1.61	-9.61	
46	208704_x_at	APLP2	-3.67	2.17E-11	3.33E-08	-1.49	-9.50	11q24
47	206940_s_at	POU4F1	-40.38	1.44E-09	5.60E-07	-1.84	-9.45	13q21.1-q22
48	226285_at	M11S1	2.14	1.97E-09	6.23E-07	1.60	9.42	11p13
49	239214_at		25.84	7.01E-08	8.40E-06	2.17	9.33	
50	49111_at		-2.35	1.41E-11	2.42E-08	-1.44	-9.32	
2.10	ALL_MLL versus CLL							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	225927_at		-5.82	8.36E-27	2.00E-22	-2.92	-21.20	
2	202625_at	LYN	-5.24	2.96E-26	3.54E-22	-2.82	-20.51	8q13
3	34210_at	CDW52	-24.53	4.26E-22	1.70E-18	-2.98	-20.17	1p36

Table 2.1-2.78

4	218942_at	FLJ22055	-10.00	1.76E-23	1.40E-19	-2.57	-18.49	12q13.13
5	224838_at	FOXP1	-3.81	2.81E-22	1.34E-18	-2.53	-18.13	3p14.1
6	218029_at	FLJ13725	-5.24	1.84E-22	1.10E-18	-2.46	-17.67	16q21
7	208091_s_at	DKFZP564K0822	-15.89	7.98E-19	9.59E-16	-2.62	-16.99	7p14.1
8	204446_s_at	ALOX5	-13.33	1.29E-19	2.20E-16	-2.49	-16.95	10q11.2
9	228993_s_at	PDCD4	-2.64	5.18E-22	1.77E-18	-2.27	-16.49	10q24
10	223514_at	CARD11	-16.46	2.89E-21	6.90E-18	-2.28	-16.40	7p22
11	204192_at	CD37	-11.59	8.17E-19	9.59E-16	-2.44	-16.38	19p13-q13.4
12	200999_s_at	CKAP4	-6.39	1.48E-21	4.42E-18	-2.25	-16.31	12q24.11
13	204661_at	CDW52	-25.76	2.24E-18	2.33E-15	-2.45	-16.19	1p36
14	207616_s_at	TANK	-3.82	1.71E-21	4.54E-18	-2.20	-15.98	2q24-q31
15	201812_s_at	TOM7	-1.90	9.45E-20	1.88E-16	-2.21	-15.84	7p15.3
16	225314_at	MGC45416	-4.77	2.78E-20	6.05E-17	-2.19	-15.72	4p11
17	212593_s_at	PDCD4	-5.73	4.23E-19	5.94E-16	-2.22	-15.57	10q24
18	224709_s_at	SPEC2	-3.28	8.42E-19	9.59E-16	-2.13	-15.21	5q31.1
19	44790_s_at	C13orf18	-59.06	4.94E-17	2.11E-14	-2.43	-15.18	13q14.11
20	236301_at		-12.99	9.17E-18	6.64E-15	-2.24	-15.15	
21	219471_at	C13orf18	-46.18	6.14E-17	2.49E-14	-2.42	-15.08	13q14.11
22	223391_at	SGPP1	-13.05	3.77E-18	3.47E-15	-2.18	-15.07	14q23.1
23	201462_at	KIAA0193	-26.17	5.60E-17	2.35E-14	-2.36	-15.01	7p14.3-p14.1
24	212313_at	MGC29816	-5.88	3.92E-19	5.86E-16	-2.07	-14.80	8p21.2
25	204798_at	MYB	35.03	8.02E-11	3.45E-09	3.24	14.78	6q22-q23
26	208296_x_at	GG2-1	-5.17	1.22E-19	2.20E-16	-1.99	-14.47	5q23.1
27	204912_at	IL10RA	-7.46	2.56E-17	1.28E-14	-2.11	-14.43	11q23
28	232950_s_at	NIR3	-6.53	2.72E-17	1.32E-14	-2.10	-14.37	12q24.31
29	239287_at		-36.96	2.86E-16	8.53E-14	-2.30	-14.33	
30	204269_at	PIM2	-4.55	2.94E-18	2.81E-15	-2.01	-14.26	Xp11.23
31	213309_at	PLCL2	-8.62	1.37E-17	8.20E-15	-2.05	-14.26	3p24.3
32	210024_s_at	UBE2E3	-6.64	2.67E-19	4.26E-16	-1.96	-14.23	2q32.1
33	212386_at		-9.76	2.11E-17	1.13E-14	-2.04	-14.16	
34	220987_s_at	SNARK	-5.13	1.21E-17	7.67E-15	-1.99	-14.03	1q32.1
35	210754_s_at	LYN	-4.48	8.40E-18	6.48E-15	-1.98	-13.99	8q13
36	205192_at	MAP3K14	-4.48	9.27E-18	6.64E-15	-1.96	-13.91	17q21
37	236248_x_at		-5.73	6.06E-19	8.04E-16	-1.91	-13.91	
38	206337_at	CCR7	-12.80	8.78E-17	3.37E-14	-2.02	-13.84	17q12-q21.2
39	213142_x_at	LOC54103	-25.43	6.09E-16	1.64E-13	-2.13	-13.77	7q11.23
40	236280_at		-11.10	1.48E-16	5.06E-14	-2.02	-13.77	
41	204949_at	ICAM3	-8.77	1.52E-16	5.11E-14	-2.01	-13.72	19p13.3-p13.2
42	228390_at		-12.86	3.26E-17	1.50E-14	-1.95	-13.71	
43	214172_x_at	RYK	-4.53	1.78E-18	1.93E-15	-1.89	-13.71	3q22
44	204512_at	HIVEP1	-7.62	1.39E-16	4.82E-14	-2.00	-13.69	6p24-p22.3
45	210425_x_at	GOLGIN-67	-12.13	9.78E-16	2.49E-13	-2.11	-13.60	15q11.2
46	229844_at		-4.86	1.22E-17	7.67E-15	-1.90	-13.59	
47	202853_s_at	RYK	-7.55	5.89E-17	2.43E-14	-1.93	-13.53	3q22
48	202863_at	SP100	-3.09	2.55E-18	2.54E-15	-1.86	-13.52	2q37.1
49	218191_s_at	FLJ11240	-2.81	1.62E-17	9.46E-15	-1.87	-13.45	6q12

Table 2.1-2.78

50	202524_s_at	SPOCK2	-6.84	1.73E-17	9.82E-15	-1.88	-13.44	10pter-q25.3
2.11	ALL_MLL versus CML							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	206871_at	ELA2	-16.25	2.58E-38	5.77E-34	-3.61	-29.24	19p13.3
2	205557_at	BPI	-13.59	1.33E-35	1.49E-31	-3.36	-27.06	20q11.23-q12
3	203949_at	MPO	-19.24	3.90E-35	2.91E-31	-3.37	-26.99	17q23.1
4	210254_at	MS4A3	-10.27	1.94E-33	1.09E-29	-3.01	-24.36	11q12
5	214575_s_at	AZU1	-35.47	2.10E-29	3.62E-26	-3.19	-24.18	19p13.3
6	225386_s_at	LOC92906	-17.75	4.72E-32	1.76E-28	-3.02	-24.11	2p22.2
7	211657_at	CEACAM6	-14.13	2.95E-31	9.41E-28	-2.91	-23.24	19q13.2
8	201554_x_at	GYG	-6.75	3.62E-29	5.40E-26	-2.94	-22.87	3q24-q25.1
9	206676_at	CEACAM8	-10.48	2.50E-32	1.12E-28	-2.80	-22.73	19q13.2
10	203948_s_at	MPO	-33.56	3.69E-28	3.75E-25	-2.99	-22.66	17q23.1
11	205653_at	CTSG	-20.45	2.84E-28	3.03E-25	-2.94	-22.49	14q11.2
12	200654_at	P4HB	-3.85	5.88E-28	5.48E-25	-2.83	-22.40	17q25
13	212268_at	SERPINB1	-3.45	1.13E-29	2.42E-26	-2.79	-22.36	6p25
14	203757_s_at	CEACAM6	-18.56	1.21E-29	2.42E-26	-2.81	-22.24	19q13.2
15	201425_at	ALDH2	-11.39	1.43E-28	1.60E-25	-2.75	-21.63	12q24.2
16	203021_at	SLPI	-11.88	1.19E-28	1.40E-25	-2.75	-21.63	20q12
17	210140_at	CST7	-8.07	4.40E-30	1.23E-26	-2.63	-21.26	20p11.21
18	204949_at	ICAM3	-16.41	1.95E-26	1.37E-23	-2.70	-20.60	19p13.3-p13.2
19	211275_s_at	GYG	-4.57	8.60E-30	2.14E-26	-2.53	-20.55	3q24-q25.1
20	205513_at	TCN1	-12.50	5.72E-27	4.57E-24	-2.61	-20.39	11q11-q12
21	204852_s_at	PTPN7	-5.07	1.30E-29	2.42E-26	-2.50	-20.33	1q32.1
22	223423_at	GPCR1	-7.85	6.20E-29	8.15E-26	-2.52	-20.30	3q26.2-q27
23	208308_s_at	GPI	-4.58	3.12E-29	4.99E-26	-2.49	-20.23	19q13.1
24	205786_s_at	ITGAM	-10.19	1.83E-27	1.58E-24	-2.56	-20.22	16p11.2
25	204971_at	CSTA	-9.57	5.88E-29	8.15E-26	-2.48	-20.09	3q21
26	200871_s_at	PSAP	-5.32	9.20E-29	1.14E-25	-2.47	-19.97	10q21-q22
27	224918_x_at	MGST1	-35.76	6.06E-25	3.15E-22	-2.69	-19.76	12p12.3-p12.1
28	225782_at	LOC253827	-27.36	2.52E-25	1.48E-22	-2.58	-19.61	12q14.1
29	206111_at	RNASE2	-7.47	6.12E-27	4.72E-24	-2.42	-19.45	14q24-q31
30	217762_s_at	RAB31	-28.14	8.55E-25	4.25E-22	-2.58	-19.32	18p11.3
31	223120_at	MGC1314	-4.11	4.82E-28	4.69E-25	-2.37	-19.23	6q24
32	200832_s_at	SCD	-20.45	1.97E-26	1.37E-23	-2.41	-19.13	10q23-q24
33	222764_at	ASRGL1	-15.26	1.46E-26	1.09E-23	-2.40	-19.07	11q12.2
34	208771_s_at	LTA4H	-5.28	3.91E-27	3.24E-24	-2.35	-18.89	12q22
35	207802_at	SGP28	-20.64	9.90E-25	4.71E-22	-2.44	-18.73	6p12.3
36	205863_at	S100A12	-7.23	1.40E-27	1.25E-24	-2.31	-18.71	1q21
37	217764_s_at	RAB31	-16.98	9.63E-25	4.68E-22	-2.43	-18.68	18p11.3
38	210244_at	CAMP	-14.11	1.64E-25	1.02E-22	-2.36	-18.62	3p21.3
39	231736_x_at	MGST1	-26.96	1.14E-23	3.81E-21	-2.50	-18.42	12p12.3-p12.1
40	208699_x_at	TKT	-5.13	6.68E-26	4.39E-23	-2.24	-18.10	3p14.3

Table 2.1-2.78

41	205237_at	FCN1	-19.53	1.06E-23	3.67E-21	-2.38	-18.07	9q34
42	212531_at	LCN2	-6.66	1.46E-23	4.72E-21	-2.27	-17.96	9q34
43	218942_at	FLJ22055	-10.48	3.73E-26	2.53E-23	-2.22	-17.92	12q13.13
44	201012_at	ANXA1	-4.29	4.44E-24	1.69E-21	-2.25	-17.92	9q12-q21.2
45	209772_s_at	CD24	-11.66	1.11E-24	5.07E-22	-2.27	-17.91	6q21
46	208637_x_at	ACTN1	-9.64	3.61E-24	1.39E-21	-2.27	-17.75	14q24
47	209369_at	ANXA3	-18.19	9.70E-24	3.44E-21	-2.30	-17.74	4q13-q22
48	201905_s_at	HYA22	-8.78	6.02E-25	3.15E-22	-2.21	-17.60	3p21.3
49	208700_s_at	TKT	-3.85	1.68E-23	5.35E-21	-2.22	-17.59	3p14.3
50	207269_at	DEFA4	-7.43	2.82E-24	1.15E-21	-2.19	-17.52	8p23
2.12	ALL_MLL versus normalBM							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	223280_x_at	MS4A6A	-14.56	3.06E-08	8.88E-06	-4.28	-16.97	11q12.1
2	201425_at	ALDH2	-10.01	8.93E-08	1.72E-05	-4.05	-15.65	12q24.2
3	202382_s_at	GNPI	-11.48	1.46E-08	5.75E-06	-3.64	-15.58	5q21
4	218257_s_at	UGCGL1	-2.61	2.17E-13	3.86E-09	-3.03	-15.36	2q14.3
5	206488_s_at	CD36	-9.24	4.46E-08	1.18E-05	-3.32	-14.14	7q11.2
6	205051_s_at	KIT	-7.11	9.04E-08	1.72E-05	-3.39	-14.00	4q11-q12
7	200832_s_at	SCD	-11.72	1.74E-08	6.05E-06	-3.15	-13.94	10q23-q24
8	224356_x_at	MS4A6A	-13.84	4.22E-07	4.82E-05	-3.75	-13.75	11q12.1
9	218424_s_at	TSAP6	-4.44	1.25E-11	1.10E-07	-2.75	-13.72	2q14.1
10	226496_at	FLJ22611	11.98	2.34E-10	4.53E-07	3.03	13.53	9p12
11	201876_at	PON2	-5.05	3.69E-10	5.46E-07	-2.73	-13.24	7q21.3
12	201858_s_at	PRG1	-3.56	6.80E-11	2.98E-07	-2.67	-13.22	10q22.1
13	205624_at	CPA3	-11.15	5.30E-07	5.47E-05	-3.48	-13.07	3q21-q25
14	217047_s_at	FAM13A1	-3.84	6.82E-10	7.56E-07	-2.70	-13.04	4q22.1
15	201988_s_at	CREBL2	-2.83	2.56E-10	4.53E-07	-2.65	-12.95	12p13
16	200871_s_at	PSAP	-6.96	7.02E-07	6.48E-05	-3.39	-12.69	10q21-q22
17	219013_at	GALNT11	-6.75	1.86E-07	2.79E-05	-3.03	-12.67	7q34-q36
18	232098_at		-6.28	4.07E-08	1.11E-05	-2.81	-12.54	
19	223120_at	MGC1314	-3.18	5.86E-09	3.15E-06	-2.67	-12.53	6q24
20	202443_x_at	NOTCH2	-4.88	1.17E-10	3.46E-07	-2.49	-12.40	1p13-p11
21	203535_at	S100A9	-4.41	5.76E-09	3.15E-06	-2.54	-12.04	1q21
22	206871_at	ELA2	-15.53	1.38E-06	9.69E-05	-3.17	-11.78	19p13.3
23	203373_at	SOCS2	23.63	2.64E-09	2.13E-06	2.77	11.76	12q
24	226556_at		-2.78	8.39E-11	2.98E-07	-2.26	-11.44	
25	208146_s_at	CPVL	-16.00	2.15E-06	1.26E-04	-3.18	-11.42	7p15-p14
26	222736_s_at	FLJ10493	-2.40	5.37E-11	2.98E-07	-2.24	-11.38	9q31.2
27	204852_s_at	PTPN7	-3.70	1.16E-07	2.06E-05	-2.54	-11.35	1q32.1
28	225703_at	KIAA1545	3.73	4.04E-10	5.51E-07	2.27	11.20	12q24.33
29	225563_at	LOC255967	5.07	1.40E-09	1.37E-06	2.33	11.12	13q12.13
30	217800_s_at	NDFIP1	-9.54	1.56E-06	1.06E-04	-2.83	-11.06	5q31.3
31	218486_at		-9.12	2.13E-06	1.26E-04	-2.94	-11.05	

Table 2.1-2.78

32	212481_s_at	TPM4	4.54	1.52E-09	1.42E-06	2.31	11.03	19p13.1
33	201417_at		6.27	3.85E-09	2.55E-06	2.40	11.00	
34	212967_x_at	NAP1L1	1.64	1.97E-10	4.53E-07	2.18	10.97	12q21.1
35	210547_x_at	ICA1	-4.80	6.80E-07	6.35E-05	-2.61	-10.95	7p22
36	212989_at	MOB	-4.36	8.75E-08	1.70E-05	-2.38	-10.90	10q
37	201506_at	TGFBI	-41.50	4.26E-06	1.86E-04	-3.37	-10.89	5q31
38	203645_s_at	CD163	-11.08	5.02E-07	5.42E-05	-2.54	-10.89	12p13.3
39	224975_at	NFIA	-5.66	6.38E-08	1.44E-05	-2.35	-10.88	1p31.3-p31.2
40	202973_x_at	FAM13A1	-4.36	6.37E-08	1.44E-05	-2.35	-10.87	4q22.1
41	228716_at		-4.10	3.66E-10	5.46E-07	-2.15	-10.85	
42	202018_s_at	LTF	-3.55	2.46E-10	4.53E-07	-2.13	-10.79	3q21-q23
43	227388_at		-3.91	1.85E-08	6.21E-06	-2.24	-10.71	
44	212207_at	KIAA1025	3.90	5.47E-10	6.93E-07	2.15	10.69	12q24.22
45	215537_x_at	DDAH2	6.41	7.88E-10	8.22E-07	2.16	10.68	6p21.3
46	208690_s_at	PDLIM1	4.27	1.82E-09	1.61E-06	2.20	10.66	10q22-q26.3
47	203796_s_at	BCL7A	11.67	4.18E-09	2.55E-06	2.25	10.60	12q24.13
48	221969_at	PAX5	8.55	7.33E-09	3.33E-06	2.26	10.45	9p13
49	214575_s_at	AZU1	-26.20	5.57E-06	2.13E-04	-3.08	-10.39	19p13.3
50	223168_at	ARHU	-6.94	3.09E-06	1.54E-04	-2.72	-10.39	1q42.11-q42.3
2.13	ALL_Ph+ versus ALL_T-lineage							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	211990_at	HLA-DPA1	7.91	5.76E-20	1.71E-15	2.61	17.41	6p21.3
2	209619_at	CD74	8.32	2.98E-16	4.43E-12	2.16	14.17	5q32
3	213539_at	CD3D	-32.29	2.13E-12	2.11E-08	-2.72	-13.85	11q23
4	210982_s_at	HLA-DRA	19.25	2.35E-10	7.94E-07	1.96	10.65	6p21.3
5	217478_s_at	HLA-DMA	11.29	2.98E-10	8.36E-07	1.90	10.47	6p21.3
6	208894_at	HLA-DRA	19.28	7.27E-10	1.44E-06	1.89	10.10	6p21.3
7	204670_x_at	HLA-DRB5	8.44	3.09E-10	8.36E-07	1.70	10.00	6p21.3
8	227584_at		9.85	9.47E-10	1.65E-06	1.86	9.96	
9	202113_s_at	SNX2	3.52	2.41E-10	7.94E-07	1.61	9.78	5q23
10	222895_s_at	BCL11B	-16.74	1.54E-09	2.17E-06	-1.85	-9.75	14q32.31
11	202789_at		-3.31	5.19E-11	3.08E-07	-1.52	-9.71	
12	201137_s_at	HLA-DPB1	11.82	1.10E-09	1.71E-06	1.72	9.66	6p21.3
13	209771_x_at	CD24	8.10	4.78E-10	1.09E-06	1.57	9.50	6q21
14	211991_s_at	HLA-DPA1	23.80	2.54E-09	2.90E-06	1.79	9.48	6p21.3
15	225314_at	MGC45416	-3.27	1.91E-10	7.94E-07	-1.50	-9.42	4p11
16	216379_x_at	KIAA1919	8.98	1.09E-09	1.71E-06	1.58	9.33	6q22
17	208306_x_at	HLA-DRB4	10.10	2.46E-09	2.90E-06	1.58	9.11	6p21.3
18	238376_at		2.91	8.49E-10	1.58E-06	1.48	9.07	
19	201160_s_at	CSDA	2.42	2.50E-11	1.86E-07	1.35	9.05	12p13.1
20	201161_s_at	CSDA	3.75	7.52E-11	3.72E-07	1.37	9.04	12p13.1
21	209604_s_at	GATA3	-8.16	4.50E-09	4.05E-06	-1.60	-8.98	10p15
22	209312_x_at	HLA-DRB1	8.50	3.16E-09	3.24E-06	1.52	8.90	6p21.3

Table 2.1-2.78

23	206804_at	CD3G	-35.77	1.26E-08	8.31E-06	-1.73	-8.74	11q23
24	217979_at	NET-6	6.22	2.00E-09	2.58E-06	1.42	8.71	7p21.1
25	224772_at	NAV1	10.79	1.37E-08	8.31E-06	1.66	8.65	
26	212998_x_at	HLA-DQB1	27.15	1.46E-08	8.32E-06	1.63	8.59	6p21.3
27	229487_at		10.71	1.25E-08	8.31E-06	1.55	8.55	
28	203932_at	HLA-DMB	8.22	1.57E-08	8.73E-06	1.60	8.54	6p21.3
29	229280_s_at		-4.99	3.07E-09	3.24E-06	-1.38	-8.52	
30	210349_at	CAMK4	-3.93	8.10E-09	6.50E-06	-1.45	-8.47	5q21.3
31	241871_at		-10.75	2.23E-08	1.05E-05	-1.63	-8.43	
32	221969_at	PAX5	7.26	7.70E-09	6.35E-06	1.42	8.42	9p13
33	238021_s_at		-8.63	1.26E-08	8.31E-06	-1.47	-8.40	
34	239081_at		-2.74	4.49E-09	4.05E-06	-1.35	-8.34	
35	215193_x_at	HLA-DRB1	13.69	2.15E-08	1.03E-05	1.53	8.34	6p21.3
36	228988_at	ZNF6	-15.56	3.09E-08	1.28E-05	-1.56	-8.23	Xq13-q21.1
37	202207_at	ARL7	-5.81	6.56E-09	5.57E-06	-1.34	-8.21	2q37.2
38	224774_s_at	NAV1	12.21	3.64E-08	1.44E-05	1.57	8.18	
39	224833_at	ETS1	-6.62	2.01E-08	9.97E-06	-1.43	-8.17	11q23.3
40	230643_at		4.79	1.68E-08	8.83E-06	1.40	8.16	
41	203133_at	SEC61B	-1.63	5.14E-10	1.09E-06	-1.20	-8.07	9q22.32-q31.3
42	201721_s_at	LAPTM5	1.98	4.58E-10	1.09E-06	1.18	8.00	1p34
43	209602_s_at	GATA3	-10.67	2.99E-08	1.27E-05	-1.39	-7.99	10p15
44	226459_at	FLJ35564	4.44	2.09E-08	1.02E-05	1.31	7.88	10q23.33
45	223046_at	EGLN1	4.79	1.03E-08	7.82E-06	1.26	7.88	1q42.1
46	229029_at		-15.16	7.55E-08	2.25E-05	-1.57	-7.87	
47	219528_s_at	BCL11B	-14.12	7.58E-08	2.25E-05	-1.52	-7.84	14q32.31
48	224909_s_at	PRex1	4.13	1.69E-08	8.83E-06	1.27	7.83	20q13.13
49	201720_s_at	LAPTM5	2.80	1.87E-09	2.53E-06	1.17	7.81	1p34
50	224773_at	NAV1	17.95	7.88E-08	2.27E-05	1.50	7.81	
2.14	ALL_Ph+ versus ALL_t(8;14)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	203373_at	SOCS2	27.49	1.43E-13	2.82E-09	2.87	15.24	12q
2	201029_s_at	CD99	4.68	5.63E-13	5.55E-09	2.05	12.02	Xp22.32
3	210487_at	DNTT	389.23	8.47E-11	4.18E-07	2.40	11.53	10q23-q24
4	201540_at	FHL1	13.44	4.17E-10	9.72E-07	1.97	10.35	Xq26
5	212012_at		19.65	2.63E-09	3.24E-06	1.88	9.52	
6	203372_s_at	SOCS2	37.37	2.86E-09	3.32E-06	1.89	9.49	12q
7	218589_at	P2RY5	16.99	2.16E-09	2.96E-06	1.80	9.48	13q14
8	223276_at	NID67	6.11	6.91E-11	4.18E-07	1.59	9.48	5q33.1
9	234107_s_at	HARS2	-5.70	4.47E-07	1.24E-04	-2.13	-9.36	20p11.23
10	202123_s_at	ABL1	3.13	4.92E-10	9.72E-07	1.63	9.35	9q34.1
11	206995_x_at	SCARF1	3.05	1.13E-10	4.44E-07	1.53	9.15	17p13.3
12	227584_at		6.35	2.25E-09	2.96E-06	1.66	9.14	
13	204663_at	ME3	3.68	3.18E-10	8.96E-07	1.53	9.05	11cen-q22.3

Table 2.1-2.78

14	217979_at	NET-6	6.58	2.18E-09	2.96E-06	1.61	9.01	7p21.1
15	226869_at		9.16	2.33E-10	7.68E-07	1.50	8.94	
16	224710_at	RAB34	6.63	4.93E-10	9.72E-07	1.51	8.90	17q11.1
17	213056_at	KIAA1013	5.45	3.07E-09	3.36E-06	1.58	8.85	3p14.1
18	210299_s_at	FHL1	14.46	9.37E-09	8.04E-06	1.72	8.83	Xq26
19	215537_x_at	DDAH2	5.36	1.14E-09	2.04E-06	1.48	8.69	6p21.3
20	223471_at	RAB3IP	-3.55	4.30E-07	1.21E-04	-1.75	-8.60	
21	228543_at	CSRP2BP	-2.06	8.67E-09	7.77E-06	-1.46	-8.43	20p11.23
22	226545_at		7.51	1.04E-08	8.53E-06	1.49	8.34	
23	212013_at	D2S448	122.63	3.25E-08	1.83E-05	1.71	8.29	2pter-p25.1
24	209530_at	CACNB3	4.71	2.13E-08	1.36E-05	1.48	8.14	12q13
25	202519_at	MONDOA	3.32	6.94E-09	6.85E-06	1.40	8.13	12q21.31
26	217870_s_at	UMP-CMPK	1.71	2.09E-09	2.96E-06	1.35	8.11	
27	219506_at	FLJ23221	4.74	1.88E-08	1.33E-05	1.45	8.07	1q21.2
28	214505_s_at	FHL1	8.53	3.46E-08	1.84E-05	1.50	8.05	Xq26
29	211709_s_at	SCGF	6.74	1.57E-08	1.19E-05	1.42	8.04	19q13.3
30	205790_at	SCAP1	-3.69	2.34E-06	3.52E-04	-1.80	-8.01	17q21.32
31	224772_at	NAV1	6.75	3.46E-08	1.84E-05	1.48	8.00	
32	210298_x_at	FHL1	22.44	5.47E-08	2.59E-05	1.56	7.98	Xq26
33	201015_s_at	JUP	14.94	3.54E-08	1.84E-05	1.45	7.94	17q21
34	223467_at	RASD1	26.47	6.28E-08	2.69E-05	1.55	7.91	17p11.2
35	209691_s_at	DOK4	16.14	7.32E-08	3.07E-05	1.53	7.84	16q12.2
36	211031_s_at	CYLN2	15.47	6.05E-08	2.66E-05	1.47	7.82	7q11.23
37	211671_s_at	NR3C1	2.93	2.00E-08	1.36E-05	1.36	7.81	5q31
38	202600_s_at	NRIP1	4.52	5.81E-09	6.03E-06	1.30	7.78	21q11.2
39	222488_s_at	DCTN4	4.33	1.38E-08	1.09E-05	1.31	7.71	5q31-q32
40	238365_s_at		5.99	8.22E-09	7.72E-06	1.29	7.68	
41	242051_at		7.08	8.77E-08	3.46E-05	1.36	7.48	
42	218694_at	ALEX1	8.11	8.24E-08	3.39E-05	1.34	7.47	Xq21.33-q22.2
43	202262_x_at	DDAH2	4.08	1.84E-08	1.33E-05	1.26	7.45	6p21.3
44	201417_at		3.68	2.15E-08	1.36E-05	1.25	7.41	
45	224833_at	ETS1	-5.24	4.00E-06	5.16E-04	-1.55	-7.34	11q23.3
46	201865_x_at	NR3C1	2.50	2.21E-08	1.36E-05	1.23	7.31	5q31
47	203853_s_at	GAB2	3.22	2.88E-08	1.67E-05	1.23	7.30	11q13.3
48	202052_s_at	RAI14	11.38	2.19E-07	7.20E-05	1.40	7.29	5p13.3-p13.2
49	219686_at	HSA250839	48.88	2.78E-07	8.83E-05	1.49	7.27	4p16.2
50	218966_at	MYO5C	4.17	1.27E-07	4.56E-05	1.31	7.27	15q21
2.15	ALL_Ph+ versus AML_MLL							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	211404_s_at	APLP2	-6.34	2.86E-19	5.76E-15	-2.13	-15.38	11q24
2	214651_s_at	HOXA9	-63.20	2.48E-16	1.67E-12	-2.45	-15.16	7p15-p14
3	208702_x_at	APLP2	-7.29	1.06E-16	1.06E-12	-1.96	-13.77	11q24
4	214875_x_at	APLP2	-7.27	2.70E-15	1.09E-11	-1.86	-12.79	11q24

Table 2.1-2.78

5	201105_at	LGALS1	-10.45	6.63E-16	3.34E-12	-1.75	-12.56	22q13.1
6	213147_at	HOXA10	-12.71	3.47E-14	1.17E-10	-1.92	-12.44	7p15-p14
7	235753_at		-12.81	1.55E-13	3.12E-10	-1.89	-11.93	
8	210487_at	DNTT	512.35	8.37E-11	2.96E-08	2.40	11.54	10q23-q24
9	206847_s_at	HOXA7	-7.12	1.84E-13	3.37E-10	-1.68	-11.35	7p15-p14
10	209905_at	HOXA9	-190.24	1.99E-12	2.20E-09	-1.87	-11.01	7p15-p14
11	234107_s_at	HARS2	-4.43	1.02E-12	1.21E-09	-1.55	-10.57	20p11.23
12	229860_x_at		-4.41	1.52E-13	3.12E-10	-1.40	-10.22	
13	223017_at	TLP19	-2.13	1.37E-13	3.12E-10	-1.37	-10.11	1p32.3
14	213150_at	HOXA10	-28.94	1.87E-11	9.69E-09	-1.64	-10.02	7p15-p14
15	218404_at	SNX10	-6.89	4.53E-12	3.81E-09	-1.47	-10.02	7p15.2
16	227584_at		9.93	1.02E-09	1.56E-07	1.89	10.01	
17	202546_at	VAMP8	-3.73	2.44E-13	4.10E-10	-1.36	-9.98	2p12-p11.2
18	217979_at	NET-6	11.37	8.31E-10	1.39E-07	1.79	9.97	7p21.1
19	205639_at	AOAH	-9.19	2.53E-12	2.47E-09	-1.41	-9.93	7p14-p12
20	200742_s_at	CLN2	-3.05	9.87E-14	2.84E-10	-1.32	-9.90	11p15
21	203733_at	MYLE	-3.78	6.12E-13	8.51E-10	-1.36	-9.90	16p13.2
22	209249_s_at	GHITM	-1.79	2.69E-13	4.17E-10	-1.32	-9.80	10q23.1
23	209771_x_at	CD24	8.90	4.78E-10	9.73E-08	1.60	9.79	6q21
24	223732_at	SLC23A2	4.96	7.65E-10	1.30E-07	1.64	9.74	5q31.2-q31.3
25	204122_at	TYROBP	-5.48	6.75E-13	8.51E-10	-1.30	-9.61	19q13.1
26	212071_s_at	SPTBN1	4.01	1.43E-10	4.17E-08	1.45	9.60	2p21
27	244084_at	FLJ30473	-5.06	9.32E-12	6.49E-09	-1.38	-9.59	22q11.21
28	223703_at	CDA017	-6.08	2.68E-11	1.23E-08	-1.45	-9.59	10q23.1
29	200803_s_at	TEGT	-2.57	2.08E-12	2.20E-09	-1.32	-9.57	12q12-q13
30	216379_x_at	KIAA1919	9.96	1.05E-09	1.58E-07	1.61	9.57	6q22
31	202054_s_at	ALDH3A2	-4.95	2.57E-12	2.47E-09	-1.31	-9.50	17p11.2
32	200743_s_at	CLN2	-2.30	6.53E-13	8.51E-10	-1.27	-9.44	11p15
33	228083_at	CACNA2D4	-11.06	1.21E-11	7.61E-09	-1.35	-9.44	12p13.33
34	217936_at		4.17	1.34E-10	4.03E-08	1.40	9.43	
35	41220_at	MSF	2.50	1.70E-10	4.89E-08	1.40	9.36	17q25
36	208608_s_at	SNTB1	-4.98	7.25E-12	5.42E-09	-1.30	-9.31	8q23-q24
37	233849_s_at	ARHGAP5	8.16	4.58E-10	9.42E-08	1.43	9.30	14q12
38	231887_s_at	KIAA1274	3.62	2.18E-09	2.61E-07	1.56	9.23	10q22.1
39	227108_at	STARD9	2.55	8.29E-10	1.39E-07	1.42	9.12	15q14
40	225745_at		3.78	6.70E-10	1.22E-07	1.40	9.12	
41	222845_x_at	CGI-119	-2.70	6.78E-12	5.26E-09	-1.23	-9.05	12q14.1-q15
42	201540_at	FHL1	6.33	1.30E-09	1.77E-07	1.43	9.05	Xq26
43	212012_at		11.97	3.68E-09	3.73E-07	1.55	9.03	
44	214430_at	GLA	-2.42	2.81E-12	2.58E-09	-1.21	-9.03	Xq22
45	201968_s_at	PGM1	-4.22	6.64E-12	5.26E-09	-1.23	-9.03	1p31
46	200886_s_at	PGAM1	-2.71	7.54E-12	5.43E-09	-1.23	-9.00	10q25.3
47	200661_at	PPGB	-4.84	1.59E-11	9.18E-09	-1.24	-8.98	20q13.1
48	227853_at		-2.96	3.25E-12	2.85E-09	-1.19	-8.93	
49	216417_x_at	HOXB9	-3.94	1.34E-11	8.20E-09	-1.22	-8.89	17q21.3

Table 2.1-2.78

50	213056_at	KIAA1013	5.12	4.98E-09	4.76E-07	1.52	8.89	3p14.1
2.16	ALL_Ph+ versus AML_inv(16)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	208702_x_at	APLP2	-6.18	2.07E-17	2.52E-13	-2.33	-15.48	11q24
2	203373_at	SOCS2	22.27	1.47E-13	2.77E-10	2.68	15.06	12q
3	208248_x_at	APLP2	-4.47	1.22E-18	2.98E-14	-2.08	-14.41	11q24
4	231310_at		-6.03	6.70E-14	1.49E-10	-2.34	-14.06	
5	211404_s_at	APLP2	-5.87	1.02E-14	5.28E-11	-2.06	-13.35	11q24
6	224918_x_at	MGST1	-10.37	4.17E-14	1.10E-10	-1.97	-12.74	12p12.3-p12.1
7	214875_x_at	APLP2	-6.83	3.12E-13	5.08E-10	-2.01	-12.55	11q24
8	205382_s_at	DF	-10.05	1.45E-14	5.28E-11	-1.86	-12.40	19p13.3
9	202746_at	ITM2A	-10.49	1.98E-12	2.10E-09	-2.11	-12.38	Xq13.3-Xq21.2
10	202747_s_at	ITM2A	-10.76	1.87E-12	2.08E-09	-2.07	-12.29	Xq13.3-Xq21.2
11	208704_x_at	APLP2	-4.46	7.98E-15	5.28E-11	-1.80	-12.17	11q24
12	231736_x_at	MGST1	-10.18	1.18E-12	1.51E-09	-1.87	-11.75	12p12.3-p12.1
13	225510_at		-6.59	4.14E-13	6.32E-10	-1.79	-11.61	
14	202720_at	TES	-5.42	1.11E-12	1.51E-09	-1.83	-11.59	7q31.2
15	204214_s_at	RAB32	-4.20	4.29E-14	1.10E-10	-1.67	-11.33	6q24.2
16	200661_at	PPGB	-4.07	1.10E-14	5.28E-11	-1.62	-11.21	20q13.1
17	233177_s_at	MR-1	-2.60	1.51E-14	5.28E-11	-1.62	-11.19	2q35
18	201497_x_at	MYH11	-25.24	5.08E-11	2.95E-08	-2.15	-11.18	16p13.13-p13.12
19	210487_at	DNTT	34.98	1.14E-10	5.37E-08	2.08	11.15	10q23-q24
20	201496_x_at	MYH11	-10.52	1.51E-11	1.15E-08	-1.87	-11.15	16p13.13-p13.12
21	207075_at	CIAS1	-5.11	2.58E-13	4.50E-10	-1.65	-11.06	1q44
22	203973_s_at	CEBPD	-4.43	4.51E-14	1.10E-10	-1.57	-10.82	8p11.2-p11.1
23	219229_at	SLC21A11	-6.75	1.30E-12	1.51E-09	-1.62	-10.72	15q26
24	217989_at	RetSDR2	-2.19	1.06E-13	2.16E-10	-1.51	-10.43	4q21.3
25	200872_at	S100A10	-6.57	3.77E-11	2.36E-08	-1.69	-10.42	1q21
26	201811_x_at	SH3BP5	8.81	2.27E-10	9.23E-08	1.81	10.39	3p24.3
27	204122_at	TYROBP	-5.91	1.27E-12	1.51E-09	-1.54	-10.35	19q13.1
28	201360_at	CST3	-9.35	1.33E-11	1.11E-08	-1.60	-10.27	20p11.21
29	226611_s_at	p30	-2.79	6.06E-13	8.71E-10	-1.48	-10.13	17p11.2
30	229776_at	SLC21A11	-2.56	2.77E-12	2.71E-09	-1.49	-10.06	15q26
31	224583_at	COTL1	-4.30	2.72E-12	2.71E-09	-1.41	-9.66	16q23.3
32	221059_s_at	CHST6	-4.22	5.93E-12	5.57E-09	-1.41	-9.59	16q22
33	227711_at	FLJ32942	-4.79	1.79E-11	1.32E-08	-1.42	-9.49	12q13.13
34	208703_s_at	APLP2	-5.68	3.93E-11	2.40E-08	-1.43	-9.46	11q24
35	203948_s_at	MPO	-4.34	2.81E-11	1.91E-08	-1.41	-9.44	17q23.1
36	220326_s_at	FLJ10357	-4.45	3.77E-10	1.28E-07	-1.52	-9.36	14q11.1
37	218017_s_at	FLJ22242	-4.09	1.05E-11	9.52E-09	-1.37	-9.35	8p11.1
38	203372_s_at	SOCS2	25.58	3.41E-09	7.12E-07	1.77	9.34	12q
39	209771_x_at	CD24	7.36	5.42E-10	1.76E-07	1.48	9.24	6q21
40	212012_at		15.84	2.48E-09	5.72E-07	1.63	9.24	

Table 2.1-2.78

41	203949_at	MPO	-3.39	3.54E-10	1.25E-07	-1.46	-9.23	17q23.1
42	224724_at	SULF2	-7.95	1.22E-09	3.36E-07	-1.58	-9.21	20q12-13.2
43	202016_at	MEST	-5.68	2.68E-10	1.07E-07	-1.44	-9.17	7q32
44	217979_at	NET-6	7.52	1.19E-09	3.31E-07	1.50	9.14	7p21.1
45	202074_s_at	OPTN	3.47	4.99E-11	2.95E-08	1.35	9.08	10p14
46	212071_s_at	SPTBN1	3.21	1.36E-09	3.65E-07	1.49	9.06	2p21
47	225579_at	MGC33602	-3.49	5.73E-10	1.82E-07	-1.44	-9.04	2p25.1
48	222942_s_at	TIAM2	6.59	2.92E-09	6.54E-07	1.55	9.02	6q25
49	216379_x_at	KIAA1919	7.87	1.24E-09	3.37E-07	1.46	9.01	6q22
50	215706_x_at	ZYX	-3.01	1.14E-11	9.98E-09	-1.30	-8.97	7q32
2.17	ALL_Ph+ versus AML_inv(3)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	210487_at	DNTT	11.52	1.27E-10	1.60E-06	1.65	9.88	10q23-q24
2	203373_at	SOCS2	4.03	7.83E-12	1.98E-07	1.52	9.72	12q
3	217963_s_at	NGFRAP1	-16.83	2.47E-08	5.67E-05	-1.94	-9.46	Xq22.1
4	234107_s_at	HARS2	-5.90	2.91E-08	5.67E-05	-1.86	-9.26	20p11.23
5	230659_at	KIAA0212	3.25	8.04E-10	6.78E-06	1.54	9.16	3p26.1
6	201462_at	KIAA0193	-9.36	2.54E-08	5.67E-05	-1.76	-9.14	7p14.3-p14.1
7	218094_s_at	C20orf35	-5.88	5.35E-08	6.54E-05	-1.68	-8.71	20q13.11
8	201243_s_at	ATP1B1	-8.09	1.31E-07	1.07E-04	-1.60	-8.24	1q22-q25
9	229487_at		7.70	2.65E-08	5.67E-05	1.53	8.23	
10	221969_at	PAX5	5.65	2.02E-08	5.67E-05	1.43	8.12	9p13
11	230643_at		4.40	2.81E-08	5.67E-05	1.44	8.04	
12	203372_s_at	SOCS2	6.50	2.33E-08	5.67E-05	1.39	7.98	12q
13	205645_at	REPS2	-4.97	5.00E-08	6.54E-05	-1.37	-7.93	Xp22.22
14	206295_at	IL18	-5.36	1.13E-07	9.66E-05	-1.40	-7.82	11q22.2-q22.3
15	204214_s_at	RAB32	-2.66	2.22E-09	1.40E-05	-1.21	-7.75	6q24.2
16	227276_at	TEM7R	-3.75	2.11E-07	1.44E-04	-1.43	-7.74	10p12.1
17	212012_at		6.16	1.36E-08	5.67E-05	1.27	7.72	
18	37408_at	MRC2	-3.20	2.44E-07	1.46E-04	-1.41	-7.64	17q23.3
19	202626_s_at	LYN	-2.97	1.20E-08	5.67E-05	-1.23	-7.63	8q13
20	219229_at	SLC21A11	-4.52	3.14E-08	5.67E-05	-1.23	-7.51	15q26
21	202439_s_at	IDS	-2.76	2.32E-07	1.46E-04	-1.33	-7.44	Xq28
22	212223_at		-2.72	1.14E-07	9.66E-05	-1.25	-7.38	
23	244623_at		-3.37	7.77E-08	8.19E-05	-1.23	-7.37	
24	207111_at	EMR1	-3.48	3.87E-07	1.85E-04	-1.35	-7.35	19p13.3
25	221558_s_at	LEF1	17.17	2.53E-07	1.46E-04	1.45	7.29	4q23-q25
26	226865_at		-7.62	7.26E-07	2.55E-04	-1.41	-7.29	
27	207655_s_at	BLNK	11.17	2.08E-07	1.44E-04	1.35	7.27	10q23.2-q23.33
28	218885_s_at	GALNT12	-3.53	4.68E-08	6.54E-05	-1.18	-7.26	9q22.33
29	227425_at		-2.60	2.69E-07	1.46E-04	-1.26	-7.21	
30	209710_at	MGC2306	-4.81	7.21E-07	2.55E-04	-1.36	-7.20	3q21.3
31	229649_at	NRXN3	11.73	2.68E-07	1.46E-04	1.36	7.20	14q31

Table 2.1-2.78

32	229572_at		-3.91	1.97E-07	1.42E-04	-1.23	-7.19	
33	206478_at	KIAA0125	-13.00	1.33E-06	3.50E-04	-1.48	-7.15	14q32.33
34	230896_at		-16.48	1.34E-06	3.50E-04	-1.44	-7.10	
35	230206_at		-4.08	1.14E-07	9.66E-05	-1.16	-7.05	
36	202123_s_at	ABL1	2.24	4.02E-08	6.54E-05	1.12	7.02	9q34.1
37	224413_s_at	BLP1	-2.31	1.64E-07	1.26E-04	-1.16	-6.99	8p11.21
38	201242_s_at	ATP1B1	-9.60	1.49E-06	3.67E-04	-1.37	-6.97	1q22-q25
39	232114_at	TRALPUSH	-4.92	6.54E-07	2.47E-04	-1.23	-6.94	3q25.1
40	225745_at		2.33	1.12E-07	9.66E-05	1.14	6.93	
41	233955_x_at	HSPC195	-2.96	2.72E-07	1.46E-04	-1.16	-6.91	5q31.3
42	216379_x_at	KIAA1919	4.02	4.53E-08	6.54E-05	1.09	6.90	6q22
43	227379_at	MGC44669	-1.77	6.40E-08	7.04E-05	-1.10	-6.90	6p22.2
44	202746_at	ITM2A	-5.83	1.54E-06	3.67E-04	-1.32	-6.88	Xq13.3-Xq21.2
45	222942_s_at	TIAM2	3.78	5.56E-08	6.54E-05	1.09	6.87	6q25
46	212221_x_at		-2.67	4.44E-07	2.01E-04	-1.17	-6.86	
47	212775_at	KIAA0657	-9.18	1.83E-06	3.97E-04	-1.34	-6.85	2q36.1
48	205997_at	ADAM28	-10.17	1.66E-06	3.78E-04	-1.28	-6.79	8p21.1
49	209771_x_at	CD24	3.60	5.69E-08	6.54E-05	1.06	6.77	6q21
50	201030_x_at	LDHB	-1.50	1.01E-07	9.66E-05	-1.08	-6.76	12p12.2-p12.1
2.18	ALL_Ph+ versus AML_komplext							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	203373_at	SOCS2	9.24	3.05E-13	1.92E-09	2.25	13.82	12q
2	213147_at	HOXA10	-5.85	3.31E-14	6.24E-10	-1.55	-11.14	7p15-p14
3	210487_at	DNTT	12.99	1.43E-10	1.50E-07	1.65	10.26	10q23-q24
4	209619_at	CD74	2.60	6.28E-12	1.97E-08	1.45	10.15	5q32
5	234107_s_at	HARS2	-4.18	3.08E-12	1.16E-08	-1.44	-10.01	20p11.23
6	200620_at	C1orf8	-1.82	1.38E-13	1.30E-09	-1.31	-9.82	1p36-p31
7	206847_s_at	HOXA7	-3.71	1.63E-12	7.69E-09	-1.28	-9.43	7p15-p14
8	205020_s_at	ARL4	-4.10	1.46E-11	3.43E-08	-1.26	-9.09	7p21-p15.3
9	203372_s_at	SOCS2	15.32	5.49E-09	1.38E-06	1.68	9.08	12q
10	214651_s_at	HOXA9	-34.12	2.17E-10	2.04E-07	-1.41	-8.91	7p15-p14
11	207332_s_at	TFRC	-2.88	2.45E-11	5.13E-08	-1.21	-8.82	3q26.2-qter
12	217963_s_at	NGFRAP1	-14.01	3.58E-10	2.75E-07	-1.33	-8.65	Xq22.1
13	218718_at	PDGFC	-14.47	6.75E-10	3.35E-07	-1.38	-8.53	4q32
14	207157_s_at	GNG5	-1.87	1.37E-11	3.43E-08	-1.13	-8.49	1p22
15	225782_at	LOC253827	-11.06	1.01E-10	1.35E-07	-1.18	-8.48	12q14.1
16	204671_s_at	ANKRD6	-2.76	5.02E-11	9.45E-08	-1.13	-8.38	6q14.2-q16.1
17	222978_at	SURF4	-2.25	1.07E-10	1.35E-07	-1.15	-8.36	9q34.2
18	202746_at	ITM2A	-6.82	6.01E-10	3.23E-07	-1.23	-8.32	Xq13.3-Xq21.2
19	51192_at	SSH-3	-3.34	8.40E-11	1.22E-07	-1.12	-8.28	11q13.1
20	223276_at	NID67	3.00	6.38E-09	1.46E-06	1.27	8.22	5q33.1
21	210648_x_at	SNX3	-1.65	5.59E-11	9.58E-08	-1.09	-8.20	6q21
22	235753_at		-5.68	8.67E-10	3.78E-07	-1.21	-8.19	

Table 2.1-2.78

23	205997_at	ADAM28	-11.00	8.55E-10	3.78E-07	-1.17	-8.10	8p21.1
24	222401_s_at	SMP1	-1.81	7.48E-11	1.17E-07	-1.08	-8.09	1p36.11
25	222229_x_at		1.50	3.91E-10	2.83E-07	1.11	8.09	
26	218224_at	PNMA1	-3.14	5.04E-10	3.13E-07	-1.12	-8.04	14q24.1
27	204214_s_at	RAB32	-4.24	4.44E-10	3.10E-07	-1.11	-8.02	6q24.2
28	235521_at	HOXA3	-6.05	1.86E-09	6.13E-07	-1.21	-8.01	7p15-p14
29	229487_at		6.95	3.10E-08	3.90E-06	1.35	8.00	
30	221969_at	PAX5	5.81	1.48E-08	2.40E-06	1.26	7.99	9p13
31	202747_s_at	ITM2A	-6.64	1.41E-09	5.21E-07	-1.17	-7.97	Xq13.3-Xq21.2
32	218364_at	LRRFIP2	-2.22	1.22E-10	1.35E-07	-1.06	-7.94	3p21.33
33	224598_at	MGAT4B	-1.91	1.16E-10	1.35E-07	-1.05	-7.93	5q35
34	222000_at		-2.03	3.66E-10	2.75E-07	-1.07	-7.88	
35	241706_at	LOC144402	-3.69	1.31E-09	5.21E-07	-1.12	-7.86	12q11
36	208691_at	TFRC	-2.65	5.42E-10	3.13E-07	-1.08	-7.86	3q26.2-qter
37	218618_s_at	FAD104	-4.25	7.06E-10	3.41E-07	-1.09	-7.86	3q26.31
38	207549_x_at	MCP	-1.72	2.02E-10	2.00E-07	-1.04	-7.83	1q32
39	208702_x_at	APLP2	-4.98	1.62E-09	5.56E-07	-1.12	-7.81	11q24
40	239328_at		3.78	2.29E-08	3.24E-06	1.22	7.80	
41	225032_at	FAD104	-3.39	2.98E-10	2.44E-07	-1.04	-7.78	3q26.31
42	220248_x_at	NSFL1C	-1.91	2.80E-10	2.40E-07	-1.03	-7.73	20
43	211404_s_at	APLP2	-4.81	2.23E-09	7.23E-07	-1.11	-7.73	11q24
44	225790_at	LOC253827	-9.82	7.80E-10	3.58E-07	-1.05	-7.72	12q14.1
45	226416_at	MGC35395	-3.14	2.77E-09	8.71E-07	-1.12	-7.72	8p23.1
46	202413_s_at	USP1	-1.79	2.67E-10	2.39E-07	-1.02	-7.71	1p32.1-p31.3
47	209905_at	HOXA9	-76.74	6.95E-09	1.49E-06	-1.26	-7.70	7p15-p14
48	209804_at	DCLRE1A	-3.87	4.91E-10	3.13E-07	-1.03	-7.70	10q25.1
49	200023_s_at - HG-U133A	EIF3S5	1.51	1.29E-09	5.21E-07	1.05	7.68	11p15.3
50	202001_s_at	NDUFA6	-1.70	7.29E-10	3.43E-07	-1.04	-7.68	22q13.2-q13.31
2.19	ALL_Ph+ versus AML_t(15;17)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	224918_x_at	MGST1	-18.86	5.23E-17	2.67E-13	-3.64	-21.22	12p12.3-p12.1
2	211990_at	HLA-DPA1	12.75	3.45E-18	3.51E-14	3.55	21.15	6p21.3
3	231736_x_at	MGST1	-19.37	2.72E-15	6.17E-12	-3.47	-19.40	12p12.3-p12.1
4	205382_s_at	DF	-21.42	7.44E-16	2.53E-12	-3.35	-19.32	19p13.3
5	214450_at	CTSW	-30.23	1.29E-13	1.55E-10	-3.45	-17.70	11q13.1
6	212953_x_at	CALR	-4.60	1.29E-14	2.40E-11	-3.01	-17.21	19p13.3-p13.2
7	203948_s_at	MPO	-7.81	1.93E-19	3.94E-15	-2.47	-16.22	17q23.1
8	209732_at	CLECSF2	36.12	3.01E-13	3.07E-10	2.98	15.23	12p13-p12
9	203373_at	SOCS2	21.12	1.78E-13	1.91E-10	2.76	15.06	12q
10	205624_at	CPA3	-55.84	5.74E-12	3.77E-09	-3.23	-14.93	3q21-q25
11	221739_at	IL27w	-2.38	5.10E-17	2.67E-13	-2.19	-14.28	19p13.3
12	208689_s_at	RPN2	-2.74	7.91E-17	3.23E-13	-2.09	-13.70	20q12-q13.1

Table 2.1-2.78

13	38487_at	STAB1	-6.72	1.43E-13	1.62E-10	-2.23	-13.55	3p21.31
14	217716_s_at	SEC61A1	-2.64	3.78E-14	5.92E-11	-2.15	-13.38	3q21.3
15	209619_at	CD74	5.93	2.22E-15	5.67E-12	2.08	13.37	5q32
16	238022_at		-7.99	2.31E-12	1.89E-09	-2.30	-13.27	
17	224839_s_at	GPT2	-33.18	4.95E-11	1.91E-08	-2.80	-13.17	16q12.1
18	210788_s_at	retSDR4	-4.68	5.15E-15	1.05E-11	-2.01	-12.91	14q22.3
19	200654_at	P4HB	-3.29	1.83E-15	5.34E-12	-1.94	-12.63	17q25
20	203949_at	MPO	-4.47	1.99E-14	3.38E-11	-1.97	-12.57	17q23.1
21	233072_at	KIAA1857	-11.57	8.06E-11	2.69E-08	-2.33	-12.24	9q34
22	217225_x_at	LOC283820	-2.43	3.77E-13	3.66E-10	-1.93	-12.09	16p13.13
23	202600_s_at	NRIP1	13.01	8.31E-12	4.70E-09	2.06	11.92	21q11.2
24	220798_x_at	FLJ11535	-6.19	1.54E-12	1.36E-09	-1.88	-11.66	19p13.3
25	221087_s_at	APOL3	4.63	3.50E-12	2.55E-09	1.89	11.48	22q13.1
26	217770_at	PIGT	-2.59	2.24E-12	1.89E-09	-1.84	-11.43	20q12-q13.12
27	210487_at	DNTT	81.93	9.68E-11	3.08E-08	2.26	11.40	10q23-q24
28	221004_s_at	ITM2C	-4.40	5.95E-14	8.66E-11	-1.72	-11.26	2q37
29	208675_s_at	DDOST	-2.80	6.89E-14	9.37E-11	-1.72	-11.22	1p36.1
30	205663_at	PCBP3	-4.29	1.17E-11	6.16E-09	-1.83	-11.15	21q22.3
31	205771_s_at	AKAP7	6.53	7.28E-12	4.50E-09	1.82	11.10	6q23
32	201666_at	TIMP1	-5.05	1.69E-11	7.82E-09	-1.81	-11.02	Xp11.3-p11.23
33	221253_s_at	MGC3178	-3.67	4.45E-11	1.79E-08	-1.85	-11.00	6p24.3
34	213491_x_at	RPN2	-2.14	1.22E-13	1.55E-10	-1.66	-10.88	20q12-q13.1
35	201596_x_at	KRT18	-11.99	3.44E-10	8.07E-08	-1.96	-10.85	12q13
36	200803_s_at	TEGT	-2.41	3.16E-12	2.39E-09	-1.69	-10.70	12q12-q13
37	238376_at		4.16	5.05E-11	1.91E-08	1.81	10.69	
38	200986_at	SERPING1	-11.43	1.31E-09	2.12E-07	-2.06	-10.58	11q12-q13.1
39	34210_at	CDW52	32.56	3.48E-10	8.07E-08	1.99	10.52	1p36
40	209771_x_at	CD24	19.65	1.28E-10	3.77E-08	1.82	10.47	6q21
41	212873_at	HA-1	3.33	2.74E-12	2.15E-09	1.62	10.40	19p13.3
42	214315_x_at	CALR	-2.74	9.34E-11	3.02E-08	-1.73	-10.39	19p13.3-p13.2
43	200977_s_at	TAX1BP1	-2.29	7.72E-12	4.63E-09	-1.63	-10.32	7p15
44	202599_s_at	NRIP1	8.82	1.14E-10	3.46E-08	1.75	10.32	21q11.2
45	201540_at	FHL1	14.05	3.35E-10	8.07E-08	1.87	10.32	Xq26
46	201553_s_at	LAMP1	-1.58	6.66E-13	6.17E-10	-1.57	-10.31	13q34
47	209831_x_at	DNASE2	-3.29	4.12E-10	8.92E-08	-1.79	-10.29	19p13.2
48	204150_at	STAB1	-7.73	7.44E-10	1.34E-07	-1.82	-10.23	3p21.31
49	225790_at	LOC253827	-14.52	2.61E-10	6.83E-08	-1.71	-10.14	12q14.1
50	208612_at	GRP58	-2.01	4.34E-12	2.95E-09	-1.56	-10.08	15q15
2.20	ALL_Ph+ versus AML_t(8;21)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	203373_at	SOCS2	8.25	1.28E-13	3.46E-09	2.09	13.13	12q
2	210487_at	DNTT	23.41	1.56E-10	3.01E-07	2.07	11.00	10q23-q24
3	218718_at	PDGFC	-14.86	7.65E-11	1.88E-07	-2.01	-10.88	4q32

Table 2.1-2.78

4	201811_x_at	SH3BP5	10.27	1.93E-10	3.47E-07	1.91	10.66	3p24.3
5	203949_at	MPO	-4.10	4.67E-13	4.21E-09	-1.51	-10.30	17q23.1
6	224918_x_at	MGST1	-9.71	2.67E-11	9.63E-08	-1.62	-10.24	12p12.3-p12.1
7	203948_s_at	MPO	-5.71	3.62E-13	4.21E-09	-1.46	-10.08	17q23.1
8	228827_at		-75.79	4.79E-10	7.19E-07	-1.96	-10.01	
9	211084_x_at	PRKCN	5.01	1.04E-10	2.35E-07	1.44	9.37	2p21
10	208248_x_at	APLP2	-3.24	3.25E-12	2.19E-08	-1.35	-9.36	11q24
11	231736_x_at	MGST1	-9.18	4.35E-10	6.91E-07	-1.51	-9.29	12p12.3-p12.1
12	208702_x_at	APLP2	-4.13	5.83E-11	1.58E-07	-1.39	-9.24	11q24
13	205529_s_at	CBFA2T1	-14.92	2.20E-09	2.13E-06	-1.72	-9.20	8q22
14	228058_at	LOC124220	-4.47	2.85E-11	9.63E-08	-1.36	-9.17	16p13.3
15	217989_at	RetSDR2	-2.05	7.56E-12	4.09E-08	-1.31	-9.10	4q21.3
16	208704_x_at	APLP2	-3.47	3.26E-11	9.78E-08	-1.33	-9.04	11q24
17	229406_at		-11.21	1.96E-09	2.04E-06	-1.56	-9.03	
18	233849_s_at	ARHGAP5	6.11	1.46E-09	1.72E-06	1.46	8.97	14q12
19	201810_s_at	SH3BP5	6.63	4.46E-09	2.82E-06	1.55	8.91	3p24.3
20	203372_s_at	SOCS2	12.34	7.28E-09	3.59E-06	1.66	8.91	12q
21	202719_s_at	TES	-4.02	2.10E-11	9.46E-08	-1.28	-8.86	7q31.2
22	209262_s_at	NR2F6	-7.53	1.56E-10	3.01E-07	-1.33	-8.83	19p13.1
23	221000_s_at	FKSG28	7.12	5.90E-09	3.26E-06	1.55	8.81	10q24.31
24	217936_at		3.78	2.78E-10	4.70E-07	1.32	8.75	
25	226545_at		9.50	6.70E-09	3.48E-06	1.54	8.75	
26	227584_at		5.15	4.49E-09	2.82E-06	1.45	8.65	
27	200023_s_at - HG-U133A	EIF3S5	1.50	1.05E-09	1.29E-06	1.33	8.60	11p15.3
28	221581_s_at	WBSCR5	10.83	1.50E-08	5.62E-06	1.60	8.57	7q11.23
29	218237_s_at	SLC38A1	5.09	9.37E-09	4.22E-06	1.47	8.50	12q12
30	225240_s_at		5.16	1.21E-08	4.95E-06	1.49	8.47	
31	222942_s_at	TIAM2	5.20	6.25E-09	3.31E-06	1.41	8.47	6q25
32	202600_s_at	NRIP1	3.15	2.57E-09	2.14E-06	1.34	8.45	21q11.2
33	223732_at	SLC23A2	3.68	2.62E-09	2.14E-06	1.33	8.41	5q31.2-q31.3
34	229487_at		8.40	2.36E-08	7.16E-06	1.61	8.39	
35	202123_s_at	ABL1	2.60	3.24E-09	2.44E-06	1.33	8.39	9q34.1
36	203568_s_at	TRIM38	2.59	1.91E-09	2.04E-06	1.30	8.36	6p21.3
37	208091_s_at	DKFZP564K0822	3.98	9.54E-10	1.23E-06	1.27	8.35	7p14.1
38	230643_at		5.18	1.13E-08	4.71E-06	1.40	8.31	
39	226169_at	LOC283105	2.68	3.89E-09	2.65E-06	1.31	8.28	11p15.3
40	223703_at	CDA017	-3.72	3.25E-09	2.44E-06	-1.31	-8.27	10q23.1
41	205528_s_at	CBFA2T1	-24.06	1.56E-08	5.70E-06	-1.53	-8.27	8q22
42	204214_s_at	RAB32	-4.40	2.32E-09	2.13E-06	-1.29	-8.26	6q24.2
43	41220_at	MSF	2.14	2.47E-09	2.14E-06	1.28	8.24	17q25
44	208146_s_at	CPVL	6.22	7.98E-09	3.79E-06	1.34	8.21	7p15-p14
45	38269_at	PRKD2	3.66	2.78E-08	7.84E-06	1.45	8.13	19q13.2
46	231887_s_at	KIAA1274	2.91	1.04E-08	4.51E-06	1.33	8.13	10q22.1
47	217979_at	NET-6	4.09	1.87E-08	6.35E-06	1.34	8.01	7p21.1
48	224772_at	NAV1	6.49	4.20E-08	1.02E-05	1.46	8.01	

Table 2.1-2.78

49	213056_at	KIAA1013	3.96	1.44E-08	5.62E-06	1.31	8.00	3p14.1
50	227041_at		3.20	3.69E-09	2.65E-06	1.23	8.00	
2.21	ALL_Ph+ versus CLL							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	225927_at		-6.49	1.81E-27	4.30E-23	-3.11	-23.10	
2	223514_at	CARD11	-20.32	1.96E-20	5.83E-17	-2.59	-18.00	7p22
3	224838_at	FOXP1	-3.26	1.97E-24	2.34E-20	-2.29	-17.57	3p14.1
4	202625_at	LYN	-4.47	9.93E-24	7.86E-20	-2.23	-17.06	8q13
5	224833_at	ETS1	-7.54	1.52E-21	5.14E-18	-2.29	-16.97	11q23.3
6	208091_s_at	DKFZP564K0822	-11.10	2.06E-18	2.57E-15	-2.51	-16.50	7p14.1
7	AFFX-HUMGAPDH/M33197_3_at - HG-U133B	GAPD	2.14	8.68E-23	5.15E-19	2.13	16.30	12p13
8	207616_s_at	TANK	-3.73	1.97E-22	9.36E-19	-2.08	-15.91	2q24-q31
9	226454_at	LOC92979	-4.72	4.92E-19	8.54E-16	-2.24	-15.89	12q13.13
10	203373_at	SOCS2	58.66	1.80E-13	2.20E-11	3.21	15.75	12q
11	218191_s_at	FLJ11240	-2.90	6.96E-22	2.75E-18	-2.02	-15.48	6q12
12	212313_at	MGC29816	-6.17	3.48E-19	7.10E-16	-2.11	-15.36	8p21.2
13	214615_at	P2RY10	-8.89	9.38E-18	7.91E-15	-2.21	-15.19	Xq21.1
14	234107_s_at	HARS2	-4.18	1.29E-19	3.41E-16	-2.01	-14.95	20p11.23
15	236280_at		-20.58	9.37E-17	3.97E-14	-2.29	-14.75	
16	201462_at	KIAA0193	-19.72	5.77E-17	2.96E-14	-2.20	-14.70	7p14.3-p14.1
17	223391_at	SGPP1	-9.86	9.67E-18	7.91E-15	-2.08	-14.70	14q23.1
18	201998_at	SIAT1	-9.74	1.27E-17	8.85E-15	-2.08	-14.64	3q27-q28
19	212590_at	RRAS2	-5.48	1.12E-17	8.59E-15	-2.01	-14.35	11p15.2
20	205192_at	MAP3K14	-4.73	4.71E-18	4.47E-15	-1.95	-14.21	17q21
21	239287_at		-27.28	3.90E-16	1.27E-13	-2.27	-14.19	
22	204192_at	CD37	-6.01	2.42E-18	2.61E-15	-1.89	-14.03	19p13-q13.4
23	206337_at	CCR7	-11.65	2.51E-16	9.02E-14	-2.10	-14.03	17q12-q21.2
24	208296_x_at	GG2-1	-4.05	3.59E-19	7.10E-16	-1.85	-13.97	5q23.1
25	219471_at	C13orf18	-12.58	1.88E-16	7.22E-14	-2.05	-13.95	13q14.11
26	225364_at	LOC200227	-3.16	5.03E-19	8.54E-16	-1.84	-13.92	20q13.11
27	44790_s_at	C13orf18	-13.54	9.19E-17	3.97E-14	-1.98	-13.88	13q14.11
28	214786_at	MAP3K1	-6.75	1.90E-17	1.22E-14	-1.90	-13.78	5q11.2
29	209061_at	SULF2	-5.16	5.54E-17	2.96E-14	-1.93	-13.78	20q12-13.2
30	213309_at	PLCL2	-6.85	3.71E-17	2.20E-14	-1.91	-13.73	3p24.3
31	228390_at		-12.05	4.06E-17	2.24E-14	-1.91	-13.73	
32	AFFX-HUMGAPDH/M33197_3_at - HG-U133A	GAPD	2.03	1.74E-18	2.29E-15	1.82	13.73	12p13
33	208456_s_at	RRAS2	-6.26	5.90E-17	2.96E-14	-1.89	-13.58	11p15.2
34	213353_at	ABCA5	-5.65	2.60E-16	9.12E-14	-1.93	-13.49	17q24.3

Table 2.1-2.78

35	209075_s_at	NIFU	-2.61	2.93E-19	6.96E-16	-1.75	-13.45	12q24.1
36	202524_s_at	SPOCK2	-5.37	1.75E-16	6.92E-14	-1.89	-13.41	10pter-q25.3
37	217939_s_at	FLJ20080	-2.21	1.21E-18	1.80E-15	-1.76	-13.37	2p13.3
38	227047_x_at	KIAA1538	-4.02	1.09E-18	1.72E-15	-1.75	-13.35	17p13.1
39	243780_at		-6.24	4.31E-18	4.27E-15	-1.77	-13.33	
40	220987_s_at	SNARK	-4.55	2.06E-17	1.29E-14	-1.80	-13.30	1q32.1
41	202626_s_at	LYN	-5.33	5.63E-18	5.14E-15	-1.77	-13.27	8q13
42	236301_at		-8.09	7.59E-18	6.68E-15	-1.75	-13.17	
43	203288_at	KIAA0355	-3.39	1.52E-18	2.13E-15	-1.71	-13.06	19q13.11
44	224516_s_at	HSPC195	-6.44	1.99E-16	7.49E-14	-1.79	-12.98	5q31.3
45	229072_at		-11.24	3.65E-16	1.22E-13	-1.80	-12.90	
46	50277_at	GGA1	-1.93	2.41E-18	2.61E-15	-1.68	-12.85	22q13.31
47	233955_x_at	HSPC195	-5.40	1.20E-16	4.84E-14	-1.74	-12.80	5q31.3
48	205484_at	SIT	-10.64	3.65E-15	8.65E-13	-1.90	-12.80	9p13-p12
49	221778_at	KIAA1718	-3.62	2.48E-17	1.51E-14	-1.70	-12.79	7q33-q35
50	205105_at	MAN2A1	-3.60	3.89E-18	4.01E-15	-1.67	-12.78	5q21-q22
2.22	ALL_Ph+ versus CML							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	225386_s_at	LOC92906	-15.36	1.70E-32	3.87E-28	-2.54	-21.52	2p22.2
2	205513_at	TCN1	-8.30	3.71E-27	4.23E-23	-2.15	-18.05	11q11-q12
3	207802_at	SGP28	-17.80	9.60E-26	5.47E-22	-2.07	-17.32	6p12.3
4	206440_at	LIN7A	-11.82	1.04E-24	2.97E-21	-2.06	-17.00	12q21
5	206207_at	CLC	-10.51	7.40E-25	2.78E-21	-2.01	-16.72	19q13.1
6	204174_at	ALOX5AP	-6.16	4.38E-26	3.33E-22	-1.97	-16.72	13q12
7	212531_at	LCN2	-5.79	5.86E-24	1.48E-20	-2.01	-16.72	9q34
8	210244_at	CAMP	-9.28	6.62E-25	2.78E-21	-1.88	-15.97	3p21.3
9	205786_s_at	ITGAM	-5.65	8.54E-25	2.78E-21	-1.86	-15.82	16p11.2
10	209369_at	ANXA3	-10.96	8.80E-24	1.87E-20	-1.84	-15.48	4q13-q22
11	211990_at	HLA-DPA1	4.01	2.00E-18	4.96E-16	1.95	15.26	6p21.3
12	224918_x_at	MGST1	-8.86	9.02E-24	1.87E-20	-1.79	-15.14	12p12.3-p12.1
13	226794_at	STXBP5	-9.46	2.55E-21	2.15E-18	-1.88	-15.14	6q24.3
14	202391_at	BASP1	-6.59	3.16E-23	6.00E-20	-1.74	-14.79	5p15.1-p14
15	205863_at	S100A12	-5.00	2.14E-22	3.05E-19	-1.75	-14.72	1q21
16	200803_s_at	TEGT	-2.53	4.54E-22	5.61E-19	-1.75	-14.65	12q12-q13
17	218857_s_at	ASRGL1	-8.29	7.68E-22	7.62E-19	-1.76	-14.64	11q12.2
18	203936_s_at	MMP9	-7.63	6.08E-23	1.07E-19	-1.72	-14.61	20q11.2-q13.1
19	228061_at	LOC90693	-4.33	9.21E-22	8.75E-19	-1.75	-14.58	7p15.3
20	231736_x_at	MGST1	-8.20	1.14E-22	1.86E-19	-1.71	-14.52	12p12.3-p12.1
21	218454_at	FLJ22662	-8.87	2.12E-22	3.05E-19	-1.72	-14.51	12p13.1
22	204669_s_at	RNF24	-4.34	5.05E-22	5.75E-19	-1.72	-14.46	20p13-p12.1
23	227769_at	GPR27	-8.51	7.58E-22	7.62E-19	-1.72	-14.40	3p21-p14
24	208438_s_at	FGR	-7.34	2.99E-22	4.01E-19	-1.71	-14.40	1p36.2-p36.1

Table 2.1-2.78

25	222764_at	ASRGL1	-6.12	4.68E-22	5.61E-19	-1.67	-14.18	11q12.2
26	219010_at	FLJ10901	-4.50	6.35E-22	6.90E-19	-1.68	-14.17	1q31.3
27	206676_at	CEACAM8	-5.70	4.08E-18	8.77E-16	-1.75	-13.97	19q13.2
28	206851_at	RNASE3	-7.64	3.74E-21	3.04E-18	-1.65	-13.91	14q24-q31
29	201968_s_at	PGM1	-5.58	1.05E-21	9.56E-19	-1.64	-13.88	1p31
30	226789_at		-3.60	4.12E-21	3.24E-18	-1.63	-13.77	
31	205557_at	BPI	-5.31	8.84E-17	1.21E-14	-1.76	-13.75	20q11.23-q12
32	203373_at	SOCS2	8.21	5.47E-13	1.98E-11	2.18	13.69	12q
33	205237_at	FCN1	-7.08	2.00E-21	1.75E-18	-1.61	-13.66	9q34
34	201029_s_at	CD99	5.64	1.31E-12	4.23E-11	2.31	13.65	Xp22.32
35	225782_at	LOC253827	-9.86	1.84E-20	1.20E-17	-1.62	-13.59	12q14.1
36	209619_at	CD74	4.47	5.03E-14	2.47E-12	1.94	13.56	5q32
37	210648_x_at	SNX3	-1.80	1.34E-19	5.99E-17	-1.63	-13.52	6q21
38	227266_s_at		-7.36	1.52E-19	6.43E-17	-1.65	-13.51	
39	225639_at	SCAP2	-9.99	4.35E-19	1.50E-16	-1.67	-13.43	7p21-p15
40	223423_at	GPCR1	-4.72	6.10E-19	1.93E-16	-1.62	-13.36	3q26.2-q27
41	200625_s_at	CAP	-2.58	7.62E-21	5.79E-18	-1.57	-13.31	1p34.1
42	226726_at	LOC129642	-4.34	1.39E-20	9.88E-18	-1.57	-13.27	2p25.2
43	227236_at	TSPAN-2	-12.94	1.56E-18	4.28E-16	-1.67	-13.26	1p12
44	234978_at	FLJ38932	-5.77	4.94E-19	1.68E-16	-1.63	-13.24	11q14.3
45	211883_x_at	CEACAM1	-8.71	7.83E-19	2.38E-16	-1.63	-13.20	19q13.2
46	210951_x_at	RAB27A	-4.39	1.29E-20	9.45E-18	-1.56	-13.19	15q15-q21.1
47	200983_x_at	CD59	-4.63	5.39E-20	3.06E-17	-1.57	-13.17	11p13
48	223703_at	CDA017	-4.37	5.90E-20	3.06E-17	-1.57	-13.16	10q23.1
49	231688_at		-5.57	6.09E-20	3.06E-17	-1.56	-13.14	
50	224707_at	ORF1-FL49	-6.65	1.67E-20	1.12E-17	-1.55	-13.13	5q31.3
2.23	ALL_Ph+ versus normalBM							
#	affy Id	HUGO name	fc	p	q	stn	t	Map Location
1	203373_at	SOCS2	18.81	3.48E-13	2.14E-09	3.04	15.14	12q
2	217988_at	HEI10	2.78	1.79E-14	3.30E-10	2.47	13.90	14q11.1
3	218257_s_at	UGCGL1	-2.67	1.02E-13	9.41E-10	-2.29	-12.94	2q14.3
4	204285_s_at	PMAIP1	8.93	6.33E-12	2.34E-08	2.30	12.32	18q21.31
5	218718_at	PDGFC	-5.78	3.75E-07	4.08E-05	-2.85	-12.21	4q32
6	218424_s_at	TSAP6	-2.97	1.20E-10	2.78E-07	-2.25	-12.14	2q14.1
7	206488_s_at	CD36	-5.12	2.42E-08	7.60E-06	-2.46	-12.03	7q11.2
8	205624_at	CPA3	-6.57	6.24E-07	5.64E-05	-2.88	-11.98	3q21-q25
9	224975_at	NFIA	-5.23	7.05E-07	6.12E-05	-2.83	-11.79	1p31.3-p31.2
10	232098_at		-5.33	1.09E-08	4.08E-06	-2.22	-11.32	
11	201029_s_at	CD99	3.75	4.98E-12	2.30E-08	2.01	11.28	Xp22.32
12	223044_at	SLC11A3	-9.84	1.70E-06	1.11E-04	-2.73	-11.01	2q32
13	202443_x_at	NOTCH2	-3.08	1.46E-09	1.68E-06	-2.06	-10.99	1p13-p11
14	203645_s_at	CD163	-9.38	8.92E-07	7.13E-05	-2.51	-10.89	12p13.3
15	209732_at	CLECSF2	4.21	1.06E-11	3.27E-08	1.94	10.87	12p13-p12

Table 2.1-2.78

16	210487_at	DNTT	18.51	1.92E-10	3.55E-07	2.13	10.86	10q23-q24
17	209806_at	HIST1H2BK	4.55	8.79E-11	2.32E-07	2.02	10.81	6p21.33
18	226448_at		-2.84	2.53E-08	7.80E-06	-2.10	-10.70	
19	208690_s_at	PDLIM1	5.82	1.75E-10	3.55E-07	1.99	10.58	10q22-q26.3
20	202018_s_at	LTF	-3.05	2.32E-10	3.80E-07	-1.90	-10.47	3q21-q23
21	218262_at	FLJ22318	-2.87	1.50E-07	2.34E-05	-2.08	-10.24	5q35.3
22	201540_at	FHL1	10.76	7.06E-10	1.00E-06	2.02	10.20	Xq26
23	223276_at	NID67	5.04	2.47E-10	3.80E-07	1.88	10.16	5q33.1
24	226806_s_at		-6.93	3.98E-06	1.84E-04	-2.58	-10.14	
25	224976_at	NFIA	-4.30	2.93E-06	1.52E-04	-2.46	-10.12	1p31.3-p31.2
26	201988_s_at	CREBL2	-2.20	1.04E-09	1.38E-06	-1.85	-10.10	12p13
27	223502_s_at	TNFSF13B	-5.19	8.48E-07	6.99E-05	-2.16	-9.96	13q32-34
28	203535_at	S100A9	-3.19	7.75E-09	3.67E-06	-1.87	-9.96	1q21
29	206845_s_at	RNF40	-2.26	1.46E-09	1.68E-06	-1.82	-9.95	16p11.2-p11.1
30	224608_s_at	MGC10540	-2.14	1.53E-08	5.46E-06	-1.89	-9.92	17q21.2
31	212531_at	LCN2	-5.27	2.13E-07	3.00E-05	-2.00	-9.86	9q34
32	223280_x_at	MS4A6A	-3.40	2.07E-09	1.91E-06	-1.81	-9.86	11q12.1
33	227230_s_at	KIAA1211	-9.59	6.57E-06	2.41E-04	-2.64	-9.85	4q12
34	219013_at	GALNT11	-3.69	1.02E-07	1.82E-05	-1.94	-9.81	7q34-q36
35	234107_s_at	HARS2	-3.95	2.88E-06	1.52E-04	-2.29	-9.77	20p11.23
36	234985_at	LOC143458	-3.12	1.09E-06	8.21E-05	-2.05	-9.54	11p13
37	230988_at		-4.92	7.55E-06	2.62E-04	-2.48	-9.53	
38	223063_at	FLJ14525	-3.49	1.23E-06	8.95E-05	-2.04	-9.47	1q42.13-q43
39	205076_s_at	CRA	-3.43	2.42E-06	1.36E-04	-2.12	-9.43	1q12-q21
40	218589_at	P2RY5	14.37	2.73E-09	2.26E-06	1.82	9.38	13q14
41	205566_at	ABHD2	-2.09	2.25E-07	3.05E-05	-1.86	-9.35	15q26.1
42	223223_at	ARV1	-2.69	9.92E-09	4.08E-06	-1.73	-9.34	1q42.2
43	203372_s_at	SOCS2	23.71	3.86E-09	2.55E-06	1.88	9.34	12q
44	219505_at	CECR1	-3.47	3.30E-08	9.26E-06	-1.76	-9.31	22q11.2
45	212012_at		13.95	3.73E-09	2.55E-06	1.82	9.28	
46	212383_at	ATP6V0A1	-2.15	2.33E-08	7.60E-06	-1.74	-9.26	17q21
47	223515_s_at	COQ3	-2.12	1.82E-09	1.87E-06	-1.66	-9.20	6q16.3
48	226751_at	DKFZP566K1924	-7.05	4.27E-06	1.89E-04	-2.13	-9.20	2p13.2
49	220966_x_at	MGC3038	5.05	3.23E-09	2.30E-06	1.72	9.11	9q34.11
50	236297_at		-3.32	1.25E-07	2.09E-05	-1.77	-9.10	
2.24	ALL_T-lineage versus ALL_t(8;14)							
#	affy Id	HUGO name	fc	p	q	stn	t	Map Location
1	201029_s_at	CD99	5.66	7.83E-18	1.39E-13	2.93	17.39	Xp22.32
2	213539_at	CD3D	14.40	2.84E-12	1.26E-08	2.45	13.12	11q23
3	201028_s_at	CD99	7.32	9.33E-12	3.32E-08	2.24	12.19	Xp22.32
4	201417_at		6.05	6.89E-13	6.13E-09	2.06	12.06	
5	201416_at	SOX4	6.61	2.05E-12	1.21E-08	1.87	11.10	6p22.3
6	220987_s_at	SNARK	-4.41	1.15E-07	3.84E-05	-2.15	-10.05	1q32.1

Table 2.1-2.78

7	242051_at		12.17	9.29E-10	2.07E-06	1.84	9.83	
8	224861_at		6.44	4.91E-11	1.46E-07	1.63	9.68	
9	209619_at	CD74	-6.53	1.31E-08	1.06E-05	-1.78	-9.60	5q32
10	224847_at		6.47	1.78E-09	2.88E-06	1.66	9.20	
11	204446_s_at	ALOX5	-7.10	8.49E-08	3.43E-05	-1.77	-9.14	10q11.2
12	225120_at		3.10	5.96E-10	1.51E-06	1.54	9.01	
13	228007_at		4.17	1.74E-09	2.88E-06	1.56	8.90	
14	204529_s_at	TOX	14.92	8.67E-09	7.83E-06	1.70	8.84	8q11.23
15	222895_s_at	BCL11B	8.78	2.56E-09	3.80E-06	1.55	8.78	14q32.31
16	204798_at	MYB	4.87	1.58E-09	2.88E-06	1.49	8.69	6q22-q23
17	229838_at	NUCB2	6.75	3.73E-09	5.11E-06	1.54	8.68	11p15.1-p14
18	209604_s_at	GATA3	7.59	4.05E-09	5.14E-06	1.52	8.62	10p15
19	228174_at		5.05	7.99E-09	7.83E-06	1.57	8.60	
20	235171_at		9.11	6.51E-09	7.23E-06	1.54	8.58	
21	226878_at		-3.72	4.68E-07	9.14E-05	-1.70	-8.45	
22	224848_at		6.04	2.30E-08	1.57E-05	1.57	8.30	
23	238021_s_at		9.80	7.56E-09	7.83E-06	1.45	8.27	
24	218267_at	CINP	-1.73	1.71E-08	1.22E-05	-1.35	-7.90	14q32.33
25	235353_at	KIAA0746	-3.96	1.28E-06	1.81E-04	-1.57	-7.79	4p15.2
26	37590_g_at		3.27	1.71E-08	1.22E-05	1.34	7.76	
27	212293_at	Nbak2	2.40	5.33E-09	6.32E-06	1.29	7.74	1p12
28	217478_s_at	HLA-DMA	-6.59	3.02E-06	2.88E-04	-1.69	-7.72	6p21.3
29	209530_at	CACNB3	5.85	7.43E-08	3.22E-05	1.45	7.72	12q13
30	224851_at		10.30	8.92E-08	3.50E-05	1.49	7.71	
31	226048_at		2.73	9.66E-09	8.18E-06	1.30	7.70	
32	206015_s_at	KIAA1041	2.05	8.80E-09	7.83E-06	1.30	7.70	1pter-q31.3
33	204639_at	ADA	7.61	7.87E-08	3.33E-05	1.45	7.69	20q12-q13.11
34	206804_at	CD3G	8.19	5.66E-08	2.96E-05	1.40	7.69	11q23
35	212462_at	MORF	2.49	1.48E-08	1.15E-05	1.30	7.65	10q22.2
36	211990_at	HLA-DPA1	-6.30	1.65E-06	1.99E-04	-1.54	-7.62	6p21.3
37	208306_x_at	HLA-DRB4	-5.63	1.05E-06	1.65E-04	-1.47	-7.58	6p21.3
38	215111_s_at	TSC22	7.26	1.16E-07	3.84E-05	1.44	7.56	13q14
39	219441_s_at	FLJ23119	-4.27	1.60E-06	1.99E-04	-1.49	-7.52	15q26.3
40	205349_at	GNA15	7.54	2.92E-08	1.73E-05	1.28	7.48	19p13.3
41	209312_x_at	HLA-DRB1	-5.25	1.31E-06	1.83E-04	-1.45	-7.48	6p21.3
42	218694_at	ALEX1	9.86	1.06E-07	3.84E-05	1.38	7.47	Xq21.33-q22.2
43	215193_x_at	HLA-DRB1	-7.22	3.33E-06	3.10E-04	-1.57	-7.46	6p21.3
44	209602_s_at	GATA3	7.21	6.74E-08	3.22E-05	1.32	7.44	10p15
45	204670_x_at	HLA-DRB5	-5.48	2.44E-06	2.58E-04	-1.50	-7.41	6p21.3
46	220320_at	FLJ22570	-3.52	1.26E-06	1.81E-04	-1.43	-7.40	5q35.3
47	207143_at	CDK6	4.18	6.73E-08	3.22E-05	1.29	7.36	7q21-q22
48	219528_s_at	BCL11B	8.45	1.56E-07	4.66E-05	1.34	7.29	14q32.31
49	228242_at		3.38	2.73E-08	1.73E-05	1.22	7.25	
50	228046_at	LOC152485	3.22	5.23E-08	2.96E-05	1.24	7.24	4q31.1

Table 2.1-2.78

2.25	ALL_T-lineage versus AML_MLL							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	200743_s_at	CLN2	-4.77	5.67E-21	1.12E-16	-2.23	-16.30	11p15
2	200742_s_at	CLN2	-7.00	1.02E-17	4.06E-14	-2.27	-15.50	11p15
3	211404_s_at	APLP2	-6.61	1.34E-19	8.86E-16	-2.06	-15.06	11q24
4	201858_s_at	PRG1	-4.82	5.66E-20	5.62E-16	-2.01	-14.88	10q22.1
5	206111_at	RNASE2	-8.04	1.49E-17	4.94E-14	-1.99	-14.17	14q24-q31
6	222698_s_at	IMPACT	-5.04	8.05E-18	4.00E-14	-1.93	-13.96	18q11.2-q12.1
7	213539_at	CD3D	32.88	1.64E-12	6.77E-10	2.51	13.78	11q23
8	208702_x_at	APLP2	-7.42	8.84E-17	2.51E-13	-1.95	-13.76	11q24
9	214651_s_at	HOXA9	-13.70	1.41E-16	2.79E-13	-1.88	-13.34	7p15-p14
10	227853_at		-5.26	1.41E-16	2.79E-13	-1.73	-12.64	
11	203799_at	BIMLEC	-10.51	7.61E-15	1.01E-11	-1.82	-12.48	2q24.2
12	204122_at	TYROBP	-12.79	3.68E-14	3.32E-11	-1.91	-12.40	19q13.1
13	210314_x_at	TNFSF13	-11.31	1.98E-14	2.19E-11	-1.85	-12.37	17p13.1
14	214430_at	GLA	-3.65	5.96E-16	9.10E-13	-1.70	-12.33	Xq22
15	201105_at	LGALS1	-10.90	4.58E-16	7.58E-13	-1.69	-12.28	22q13.1
16	200663_at	CD63	-2.82	1.07E-16	2.65E-13	-1.62	-12.08	12q12-q13
17	214875_x_at	APLP2	-6.16	3.69E-15	5.23E-12	-1.69	-12.04	11q24
18	201537_s_at	DUSP3	-3.76	2.57E-16	4.63E-13	-1.60	-11.89	17q21
19	223120_at	MGC1314	-4.76	8.27E-15	1.03E-11	-1.64	-11.73	6q24
20	202789_at		4.46	6.38E-12	1.52E-09	1.72	11.21	
21	209500_x_at	TNFSF13	-7.25	1.07E-13	8.20E-11	-1.61	-11.19	17p13.1
22	204971_at	CSTA	-12.16	3.91E-13	2.22E-10	-1.67	-11.15	3q21
23	231902_at	LOC152485	3.52	4.33E-12	1.21E-09	1.66	11.04	4q31.1
24	205640_at	ALDH3B1	-14.27	6.25E-13	3.10E-10	-1.66	-11.03	11q13
25	223158_s_at	NEK6	-4.80	5.86E-14	4.85E-11	-1.53	-10.95	9q33.3-q34.11
26	200764_s_at	CTNNA1	-3.53	1.00E-14	1.17E-11	-1.48	-10.89	5q31
27	219013_at	GALNT11	-5.92	2.03E-13	1.27E-10	-1.54	-10.80	7q34-q36
28	218109_s_at	FLJ14153	-5.11	1.40E-13	1.03E-10	-1.52	-10.79	3q25.32
29	221841_s_at		-9.87	2.42E-13	1.46E-10	-1.53	-10.74	
30	229215_at	ASCL2	-7.82	5.21E-13	2.72E-10	-1.56	-10.73	11p15.5
31	202054_s_at	ALDH3A2	-9.35	7.58E-14	6.02E-11	-1.48	-10.71	17p11.2
32	201029_s_at	CD99	2.39	3.12E-14	3.19E-11	1.44	10.60	Xp22.32
33	216041_x_at	GRN	-10.15	3.01E-12	1.02E-09	-1.61	-10.51	17q21.32
34	201416_at	SOX4	5.66	1.25E-12	5.66E-10	1.48	10.46	6p22.3
35	41220_at	MSF	2.61	9.98E-12	2.06E-09	1.54	10.43	17q25
36	223703_at	CDA017	-8.97	7.50E-12	1.73E-09	-1.68	-10.37	10q23.1
37	209905_at	HOXA9	-20.72	4.03E-12	1.21E-09	-1.56	-10.32	7p15-p14
38	226438_at		-6.26	2.39E-12	8.76E-10	-1.51	-10.27	
39	225314_at	MGC45416	3.91	4.16E-11	5.82E-09	1.56	10.24	4p11
40	210844_x_at	CTNNA1	-4.54	3.22E-14	3.19E-11	-1.37	-10.22	5q31
41	201200_at	CREG	-3.15	3.56E-14	3.32E-11	-1.37	-10.21	1q24
42	238483_at		3.84	3.52E-11	5.10E-09	1.54	10.19	
43	218217_at	RISC	-12.71	1.16E-11	2.37E-09	-1.64	-10.18	17q23.1

Table 2.1-2.78

44	200736_s_at	GPX1	-3.18	5.25E-14	4.53E-11	-1.36	-10.16	3p21.3
45	203555_at	PTPN18	-5.95	4.45E-12	1.21E-09	-1.51	-10.15	2q21.1
46	228007_at		6.31	2.97E-10	2.84E-08	1.68	10.12	
47	213187_x_at		-2.48	1.84E-13	1.22E-10	-1.36	-10.06	
48	203507_at	CD68	-3.86	1.70E-13	1.17E-10	-1.36	-10.01	17p13
49	209014_at	MAGED1	3.90	4.70E-10	3.93E-08	1.67	9.96	Xp11.23
50	211284_s_at	GRN	-10.99	1.39E-11	2.72E-09	-1.54	-9.96	17q21.32
2.26	ALL_T-lineage versus AML_inv(16)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	203949_at	MPO	-15.39	1.88E-26	4.18E-22	-4.23	-28.24	17q23.1
2	203948_s_at	MPO	-23.70	1.67E-19	1.24E-15	-3.54	-21.99	17q23.1
3	203973_s_at	CEBPD	-12.92	2.84E-18	1.01E-14	-2.80	-18.05	8p11.2-p11.1
4	211990_at	HLA-DPA1	-7.98	1.82E-20	2.02E-16	-2.53	-17.26	6p21.3
5	217478_s_at	HLA-DMA	-10.46	4.19E-15	4.66E-12	-2.56	-15.54	6p21.3
6	217989_at	RetSDR2	-3.68	3.66E-19	1.63E-15	-2.25	-15.46	4q21.3
7	208702_x_at	APLP2	-6.28	1.60E-17	3.97E-14	-2.32	-15.44	11q24
8	205382_s_at	DF	-67.41	6.20E-14	3.20E-11	-2.89	-15.29	19p13.3
9	200742_s_at	CLN2	-4.57	1.15E-16	2.32E-13	-2.28	-15.00	11p15
10	200743_s_at	CLN2	-3.42	3.25E-19	1.63E-15	-2.16	-14.94	11p15
11	209619_at	CD74	-7.93	3.17E-18	1.01E-14	-2.17	-14.82	5q32
12	215706_x_at	ZYX	-5.52	1.96E-15	2.56E-12	-2.17	-14.07	7q32
13	233177_s_at	MR-1	-3.34	9.27E-17	2.06E-13	-2.08	-14.05	2q35
14	224918_x_at	MGST1	-17.39	4.61E-14	2.85E-11	-2.25	-13.83	12p12.3-p12.1
15	209166_s_at	MAN2B1	-3.49	6.81E-15	6.07E-12	-2.15	-13.80	19cen-q13.1
16	200808_s_at	ZYX	-6.11	2.97E-14	2.14E-11	-2.21	-13.78	7q32
17	204670_x_at	HLA-DRB5	-7.86	6.32E-15	6.07E-12	-2.12	-13.71	6p21.3
18	213539_at	CD3D	23.12	2.79E-12	7.13E-10	2.70	13.68	11q23
19	208248_x_at	APLP2	-4.40	8.32E-18	2.31E-14	-1.97	-13.68	11q24
20	207075_at	CIAS1	-10.22	4.90E-14	2.94E-11	-2.16	-13.47	1q44
21	223120_at	MGC1314	-3.95	1.77E-16	3.03E-13	-1.96	-13.35	6q24
22	209312_x_at	HLA-DRB1	-9.42	4.43E-14	2.85E-11	-2.10	-13.27	6p21.3
23	208306_x_at	HLA-DRB4	-10.58	6.33E-14	3.20E-11	-2.11	-13.25	6p21.3
24	229776_at	SLC21A11	-3.56	1.45E-16	2.68E-13	-1.93	-13.23	15q26
25	200665_s_at	SPARC	-10.31	5.86E-14	3.16E-11	-2.10	-13.23	5q31.3-q32
26	204122_at	TYROBP	-13.81	7.60E-13	2.45E-10	-2.29	-13.15	19q13.1
27	211404_s_at	APLP2	-6.13	4.57E-15	4.84E-12	-1.98	-13.12	11q24
28	210982_s_at	HLA-DRA	-20.46	1.02E-12	3.08E-10	-2.27	-12.99	6p21.3
29	203799_at	BIMLEC	-10.91	3.15E-13	1.27E-10	-2.10	-12.87	2q24.2
30	38487_at	STAB1	-7.03	3.20E-15	3.75E-12	-1.91	-12.83	3p21.31
31	231736_x_at	MGST1	-17.87	9.94E-13	3.03E-10	-2.15	-12.70	12p12.3-p12.1
32	219079_at	b5	-2.51	5.30E-16	7.86E-13	-1.83	-12.59	6pter-q22.33
33	200696_s_at	GSN	-6.77	1.92E-13	8.54E-11	-1.97	-12.47	9q33
34	224391_s_at	CSE-C	-4.40	5.93E-14	3.16E-11	-1.91	-12.45	11q24

Table 2.1-2.78

35	205419_at	EBI2	-11.69	7.72E-13	2.45E-10	-2.03	-12.39	13q32.2
36	228058_at	LOC124220	-10.60	5.85E-13	2.00E-10	-2.00	-12.38	16p13.3
37	202789_at		5.57	6.05E-12	1.29E-09	2.15	12.37	
38	200736_s_at	GPX1	-3.75	3.22E-16	5.12E-13	-1.79	-12.37	3p21.3
39	217984_at	RNASE6PL	-3.08	5.11E-14	2.99E-11	-1.89	-12.37	6q27
40	221841_s_at		-10.69	1.96E-13	8.54E-11	-1.93	-12.32	
41	224252_s_at	FXYD5	-2.50	7.38E-16	1.03E-12	-1.75	-12.12	19q12-q13.1
42	218217_at	RISC	-8.28	3.57E-12	8.55E-10	-2.06	-12.09	17q23.1
43	202241_at	C8FW	-7.80	1.44E-12	4.11E-10	-1.95	-12.00	8q24.13
44	208704_x_at	APLP2	-4.51	7.38E-15	6.32E-12	-1.76	-11.95	11q24
45	201887_at	IL13RA1	-16.03	1.16E-11	2.15E-09	-2.17	-11.88	Xq24
46	225510_at		-7.12	3.44E-13	1.37E-10	-1.85	-11.88	
47	201531_at	ZFP36	-4.02	6.83E-15	6.07E-12	-1.74	-11.86	19q13.1
48	214875_x_at	APLP2	-5.79	3.12E-13	1.27E-10	-1.81	-11.74	11q24
49	201360_at	CST3	-22.30	1.06E-11	2.05E-09	-2.05	-11.71	20p11.21
50	217983_s_at	RNASE6PL	-2.82	3.51E-14	2.44E-11	-1.74	-11.70	6q27
2.27	ALL_T-lineage versus AML_inv(3)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	213539_at	CD3D	25.77	1.56E-12	2.99E-08	2.50	13.58	11q23
2	211990_at	HLA-DPA1	-7.73	1.78E-11	7.54E-08	-2.06	-11.98	6p21.3
3	209619_at	CD74	-6.38	2.35E-12	2.99E-08	-1.82	-11.22	5q32
4	201200_at	CREG	-3.83	1.02E-11	5.20E-08	-1.83	-11.10	1q24
5	228624_at	FLJ11155	-5.59	3.60E-10	7.04E-07	-1.77	-10.28	4q32.1
6	202789_at		4.14	7.45E-12	4.74E-08	1.65	10.28	
7	201888_s_at	IL13RA1	-5.36	5.76E-10	9.76E-07	-1.79	-10.26	Xq24
8	218818_at	FHL3	-2.51	3.77E-11	1.37E-07	-1.62	-10.00	1p34
9	226694_at	AKAP2	14.72	7.93E-10	1.26E-06	1.76	9.79	9q31-q33
10	201029_s_at	CD99	2.00	7.35E-12	4.74E-08	1.53	9.75	Xp22.32
11	222895_s_at	BCL11B	15.95	1.53E-09	2.05E-06	1.83	9.69	14q32.31
12	202626_s_at	LYN	-4.85	2.60E-10	6.34E-07	-1.60	-9.65	8q13
13	206295_at	IL18	-14.82	2.50E-08	1.37E-05	-1.88	-9.36	11q22.2-q22.3
14	221558_s_at	LEF1	25.64	5.65E-09	5.64E-06	1.83	9.15	4q23-q25
15	217989_at	RetSDR2	-3.39	3.93E-09	4.76E-06	-1.58	-9.14	4q21.3
16	217478_s_at	HLA-DMA	-8.47	3.59E-08	1.43E-05	-1.78	-9.05	6p21.3
17	221710_x_at	FLJ10647	-6.23	5.52E-09	5.64E-06	-1.57	-9.04	1p34.3
18	201137_s_at	HLA-DPB1	-9.95	3.13E-08	1.37E-05	-1.74	-9.02	6p21.3
19	200765_x_at	CTNNA1	-3.82	1.46E-10	4.12E-07	-1.43	-9.00	5q31
20	202759_s_at	AKAP2	8.96	4.38E-09	5.06E-06	1.60	8.91	9q31-q33
21	219582_at	FLJ21079	-2.67	6.18E-11	1.97E-07	-1.39	-8.91	6q13
22	227853_at		-3.61	1.21E-09	1.70E-06	-1.44	-8.82	
23	210349_at	CAMK4	4.22	5.64E-09	5.64E-06	1.54	8.71	5q21.3
24	204670_x_at	HLA-DRB5	-6.61	3.11E-08	1.37E-05	-1.58	-8.64	6p21.3
25	206804_at	CD3G	26.75	1.39E-08	9.44E-06	1.64	8.61	11q23

Table 2.1-2.78

26	202625_at	LYN	-4.11	5.43E-10	9.76E-07	-1.37	-8.61	8q13
27	218450_at	HEBP1	-3.28	2.74E-10	6.34E-07	-1.35	-8.58	12p13.2
28	227193_at		4.83	6.83E-09	6.44E-06	1.48	8.50	
29	221497_x_at	EGLN1	-2.90	3.48E-10	7.04E-07	-1.33	-8.48	1q42.1
30	227276_at	TEM7R	-4.87	6.47E-08	2.08E-05	-1.57	-8.41	10p12.1
31	241871_at		10.30	2.37E-08	1.34E-05	1.62	8.38	
32	228058_at	LOC124220	-4.92	7.40E-09	6.72E-06	-1.38	-8.29	16p13.3
33	209014_at	MAGED1	2.79	5.77E-09	5.64E-06	1.38	8.24	Xp11.23
34	201537_s_at	DUSP3	-3.23	1.20E-08	8.70E-06	-1.37	-8.19	17q21
35	226459_at	FLJ35564	-3.47	1.82E-08	1.16E-05	-1.38	-8.13	10q23.33
36	202760_s_at	AKAP2	13.26	2.77E-08	1.37E-05	1.48	8.13	9q31-q33
37	210844_x_at	CTNNA1	-3.60	9.89E-10	1.48E-06	-1.28	-8.12	5q31
38	205255_x_at	TCF7	9.44	4.17E-08	1.57E-05	1.58	8.12	5q31.1
39	203127_s_at	SPTLC2	-2.61	2.30E-08	1.33E-05	-1.39	-8.12	14q24.3-q31
40	209312_x_at	HLA-DRB1	-7.21	1.01E-07	2.79E-05	-1.50	-8.10	6p21.3
41	203799_at	BIMLEC	-6.76	9.40E-08	2.69E-05	-1.48	-8.07	2q24.2
42	239422_at	DKFZp547M109	4.85	1.45E-08	9.44E-06	1.38	8.07	7q22.1
43	202888_s_at	ANPEP	-4.31	1.16E-08	8.70E-06	-1.34	-8.06	15q25-q26
44	235492_at	MGC26996	-2.98	3.72E-08	1.46E-05	-1.39	-8.05	6q22.33
45	220134_x_at	FLJ10647	-3.27	3.37E-08	1.38E-05	-1.38	-8.04	1p34.3
46	208178_x_at	TRIO	-4.54	3.16E-09	4.02E-06	-1.27	-7.98	5p15.1-p14
47	214032_at	ZAP70	11.00	3.25E-08	1.38E-05	1.42	7.97	2q12
48	238469_at		-3.26	9.25E-09	7.84E-06	-1.29	-7.90	
49	229029_at		15.69	7.27E-08	2.25E-05	1.59	7.89	
50	219528_s_at	BCL11B	14.46	7.40E-08	2.27E-05	1.54	7.85	14q32.31
2.28	ALL_T-lineage versus AML_komplext							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	201200_at	CREG	-3.92	2.00E-17	3.58E-13	-1.67	-12.52	1q24
2	213539_at	CD3D	10.37	1.14E-12	1.20E-09	1.87	12.16	11q23
3	200620_at	C1orf8	-2.07	9.09E-16	8.13E-12	-1.50	-11.28	1p36-p31
4	200742_s_at	CLN2	-4.73	5.41E-13	6.91E-10	-1.51	-10.56	11p15
5	228624_at	FLJ11155	-7.60	7.45E-13	8.88E-10	-1.51	-10.48	4q32.1
6	203837_at	MAP3K5	-4.26	5.52E-14	1.77E-10	-1.40	-10.36	6q22.33
7	224598_at	MGAT4B	-2.22	4.96E-14	1.77E-10	-1.38	-10.27	5q35
8	202789_at		3.50	3.49E-11	1.49E-08	1.54	10.23	
9	227853_at		-4.03	6.29E-14	1.77E-10	-1.37	-10.21	
10	200743_s_at	CLN2	-3.43	1.41E-13	2.80E-10	-1.39	-10.21	11p15
11	226459_at	FLJ35564	-4.28	2.95E-13	5.27E-10	-1.40	-10.19	10q23.33
12	214430_at	GLA	-2.72	6.92E-14	1.77E-10	-1.35	-10.11	Xq22
13	210648_x_at	SNX3	-2.00	6.47E-14	1.77E-10	-1.32	-9.98	6q21
14	201858_s_at	PRG1	-3.90	9.85E-14	2.20E-10	-1.30	-9.85	10q22.1
15	200701_at	NPC2	-3.06	3.50E-13	5.69E-10	-1.30	-9.69	14q24.3
16	221188_s_at	CIDEB	-3.21	1.43E-12	1.34E-09	-1.32	-9.63	14q11.2

Table 2.1-2.78

17	223120_at	MGC1314	-3.28	5.01E-13	6.89E-10	-1.29	-9.61	6q24
18	226694_at	AKAP2	10.47	1.73E-09	2.17E-07	1.73	9.61	9q31-q33
19	214356_s_at	KIAA0368	-3.30	3.98E-13	5.93E-10	-1.25	-9.46	9q32
20	218364_at	LRRFIP2	-2.38	3.93E-12	3.05E-09	-1.30	-9.42	3p21.33
21	218109_s_at	FLJ14153	-3.65	1.22E-12	1.21E-09	-1.26	-9.41	3q25.32
22	207809_s_at	ATP6IP1	-2.59	1.12E-12	1.20E-09	-1.24	-9.28	Xq28
23	206111_at	RNASE2	-6.98	2.30E-11	1.21E-08	-1.33	-9.25	14q24-q31
24	200696_s_at	GSN	-4.84	1.14E-11	6.78E-09	-1.27	-9.16	9q33
25	201061_s_at	STOM	-4.96	6.20E-12	4.11E-09	-1.25	-9.15	9q34.1
26	200975_at	PPT1	-2.53	5.11E-12	3.66E-09	-1.24	-9.13	1p32
27	204249_s_at	LMO2	-4.31	1.69E-12	1.52E-09	-1.20	-9.08	11p13
28	226438_at		-4.51	2.22E-11	1.20E-08	-1.27	-9.04	
29	213798_s_at	CAP	-2.49	5.53E-12	3.81E-09	-1.22	-9.02	1p34.1
30	201443_s_at	ATP6IP2	-2.18	3.39E-12	2.76E-09	-1.20	-9.01	Xq21
31	222895_s_at	BCL11B	9.43	2.21E-09	2.58E-07	1.44	8.96	14q32.31
32	202381_at	ADAM9	-5.08	2.95E-11	1.35E-08	-1.25	-8.94	8p11.21
33	223158_s_at	NEK6	-5.73	7.96E-11	2.91E-08	-1.30	-8.93	9q33.3-q34.11
34	213187_x_at		-2.40	4.44E-12	3.31E-09	-1.18	-8.90	
35	205418_at	FES	-8.59	2.90E-11	1.35E-08	-1.24	-8.89	15q26.1
36	202263_at	CYB5R1	-2.23	3.29E-12	2.76E-09	-1.18	-8.89	1p36.13-q41
37	201029_s_at	CD99	1.92	1.14E-11	6.78E-09	1.20	8.88	Xp22.32
38	210145_at	PLA2G4A	-8.10	1.91E-10	4.79E-08	-1.35	-8.84	1q25
39	201060_x_at	STOM	-5.93	3.71E-11	1.55E-08	-1.23	-8.84	9q34.1
40	203836_s_at	MAP3K5	-6.13	3.22E-11	1.43E-08	-1.23	-8.83	6q22.33
41	225059_at	AGTRAP	-7.31	1.20E-10	3.71E-08	-1.28	-8.80	1p36.21
42	213066_at	KIAA0375	-6.14	2.37E-10	5.30E-08	-1.31	-8.72	9p13.1
43	202241_at	C8FW	-7.80	2.40E-10	5.30E-08	-1.30	-8.69	8q24.13
44	227185_at		-2.67	8.80E-11	3.02E-08	-1.22	-8.67	
45	203041_s_at	LAMP2	-4.07	9.10E-11	3.02E-08	-1.22	-8.66	Xq24
46	210613_s_at	SYNGR1	-7.61	1.38E-10	4.10E-08	-1.24	-8.66	22q13.1
47	221558_s_at	LEF1	12.45	1.00E-08	7.57E-07	1.52	8.65	4q23-q25
48	227999_at	LOC170394	-3.04	8.41E-12	5.37E-09	-1.14	-8.63	10q26.3
49	207980_s_at	CITED2	-4.65	1.57E-10	4.53E-08	-1.24	-8.62	6q23.3
50	202252_at	RAB13	-3.79	2.19E-11	1.20E-08	-1.15	-8.59	1q21.2
2.29	ALL_T-lineage versus AML_t(15;17)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	203949_at	MPO	-20.28	1.41E-20	2.64E-16	-4.90	-28.93	17q23.1
2	203948_s_at	MPO	-42.61	3.90E-17	1.46E-13	-4.88	-25.92	17q23.1
3	224918_x_at	MGST1	-31.61	2.51E-16	5.87E-13	-4.06	-22.36	12p12.3-p12.1
4	205382_s_at	DF	-143.63	1.00E-14	1.11E-11	-4.55	-21.22	19p13.3
5	231736_x_at	MGST1	-34.01	6.64E-15	8.89E-12	-3.87	-20.28	12p12.3-p12.1
6	206871_at	ELA2	-14.98	1.02E-17	4.80E-14	-3.31	-20.10	19p13.3

Table 2.1-2.78

7	206111_at	RNASE2	-8.11	4.22E-18	2.64E-14	-2.98	-18.60	14q24-q31
8	200654_at	P4HB	-3.92	2.83E-19	2.65E-15	-2.92	-18.60	17q25
9	212953_x_at	CALR	-5.70	2.18E-15	4.09E-12	-3.07	-17.91	19p13.3-p13.2
10	38487_at	STAB1	-55.71	3.99E-13	3.12E-10	-3.58	-17.21	3p21.31
11	214450_at	CTSW	-15.45	5.37E-14	5.26E-11	-2.96	-16.63	11q13.1
12	214575_s_at	AZU1	-48.06	9.33E-13	5.58E-10	-3.32	-16.29	19p13.3
13	200663_at	CD63	-3.32	1.45E-16	3.87E-13	-2.39	-15.20	12q12-q13
14	209215_at	TETRAN	-6.30	3.23E-13	2.63E-10	-2.36	-13.96	4p16.3
15	213854_at	SYNGR1	-5.75	7.86E-15	9.83E-12	-2.22	-13.94	22q13.1
16	205624_at	CPA3	-19.90	1.76E-12	8.91E-10	-2.44	-13.83	3q21-q25
17	208689_s_at	RPN2	-2.58	5.45E-17	1.70E-13	-2.10	-13.79	20q12-q13.1
18	202789_at		8.98	1.45E-12	7.77E-10	2.44	13.49	
19	231902_at	LOC152485	5.52	9.25E-13	5.58E-10	2.33	13.34	4q31.1
20	208675_s_at	DDOST	-3.19	4.12E-15	7.03E-12	-2.09	-13.34	1p36.1
21	218084_x_at	FXYD5	-2.51	3.51E-16	7.30E-13	-1.99	-13.07	19q12-q13.1
22	208612_at	GRP58	-2.71	6.15E-15	8.87E-12	-2.01	-12.89	15q15
23	208852_s_at	CANX	-3.42	5.76E-13	4.00E-10	-2.12	-12.87	5q35
24	221004_s_at	ITM2C	-4.81	1.01E-14	1.11E-11	-2.00	-12.83	2q37
25	210613_s_at	SYNGR1	-10.53	8.63E-12	3.30E-09	-2.25	-12.76	22q13.1
26	204347_at	AK3	-10.69	1.27E-11	4.50E-09	-2.26	-12.68	1p31.3
27	201858_s_at	PRG1	-3.94	4.88E-15	7.62E-12	-1.87	-12.22	10q22.1
28	225286_at		-6.16	1.36E-12	7.52E-10	-2.00	-12.20	
29	221253_s_at	MGC3178	-4.90	7.89E-12	3.08E-09	-2.06	-12.12	6p24.3
30	220798_x_at	FLJ11535	-5.89	4.86E-12	2.19E-09	-2.03	-12.10	19p13.3
31	216032_s_at	SDBCAG84	-3.02	5.61E-14	5.26E-11	-1.88	-12.05	20pter-q12
32	201136_at	PLP2	-4.55	3.03E-12	1.42E-09	-1.99	-12.02	Xp11.23
33	204150_at	STAB1	-58.82	2.45E-10	4.56E-08	-2.57	-12.01	3p21.31
34	225314_at	MGC45416	5.49	2.05E-11	6.31E-09	2.15	11.88	4p11
35	203591_s_at	CSF3R	-10.25	3.71E-11	1.03E-08	-2.10	-11.88	1p35-p34.3
36	201596_x_at	KRT18	-23.28	3.63E-10	5.96E-08	-2.42	-11.66	12q13
37	221739_at	IL27w	-2.05	1.49E-14	1.56E-11	-1.78	-11.65	19p13.3
38	201360_at	CST3	-17.88	1.64E-10	3.26E-08	-2.18	-11.63	20p11.21
39	228625_at	CITED4	-3.98	1.63E-12	8.51E-10	-1.87	-11.62	1p34.1
40	217225_x_at	LOC283820	-2.35	5.76E-13	4.00E-10	-1.83	-11.58	16p13.13
41	200714_x_at	OS-9	-2.84	2.08E-12	1.00E-09	-1.85	-11.49	12q13
42	200649_at	NUCB1	-4.29	2.48E-11	7.39E-09	-1.95	-11.46	19q13.2-q13.4
43	228007_at		14.37	7.23E-11	1.83E-08	2.17	11.44	
44	39854_r_at	TTS-2.2	-3.12	6.44E-11	1.68E-08	-1.99	-11.40	11p15.5
45	201666_at	TIMP1	-5.85	7.37E-12	2.94E-09	-1.86	-11.34	Xp11.3-p11.23
46	203471_s_at	PLEK	-5.03	1.71E-11	5.45E-09	-1.88	-11.28	2p13.2
47	209166_s_at	MAN2B1	-3.78	1.48E-10	3.03E-08	-2.00	-11.20	19cen-q13.1
48	211934_x_at	G2AN	-4.29	3.41E-11	9.68E-09	-1.89	-11.19	11q12.2
49	210788_s_at	retSDR4	-2.92	8.10E-13	5.24E-10	-1.75	-11.15	14q22.3
50	210140_at	CST7	-16.06	7.10E-10	9.51E-08	-2.25	-11.13	20p11.21

Table 2.1-2.78

2.30	ALL_T-lineage versus AML_t(8;21)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	203949_at	MPO	-18.61	2.14E-18	4.79E-14	-3.33	-20.45	17q23.1
2	203948_s_at	MPO	-31.15	2.42E-14	7.74E-11	-2.70	-15.40	17q23.1
3	217989_at	RetSDR2	-3.45	2.21E-17	2.47E-13	-2.03	-13.89	4q21.3
4	213539_at	CD3D	23.17	1.72E-12	2.57E-09	2.44	13.52	11q23
5	217478_s_at	HLA-DMA	-7.27	5.46E-14	1.53E-10	-2.10	-13.23	6p21.3
6	211990_at	HLA-DPA1	-7.06	2.80E-15	1.59E-11	-1.93	-12.94	6p21.3
7	204604_at	PFTK1	-4.19	1.97E-14	7.35E-11	-1.85	-12.32	7q21-q22
8	228058_at	LOC124220	-12.47	1.45E-12	2.31E-09	-2.05	-12.30	16p13.3
9	209545_s_at	RIPK2	-5.07	2.84E-15	1.59E-11	-1.71	-11.81	8q21
10	209619_at	CD74	-6.36	7.64E-15	3.42E-11	-1.71	-11.69	5q32
11	210613_s_at	SYNGR1	-10.58	3.76E-12	4.21E-09	-1.91	-11.63	22q13.1
12	200743_s_at	CLN2	-3.62	2.07E-13	4.64E-10	-1.70	-11.31	11p15
13	200696_s_at	GSN	-7.92	8.43E-12	8.73E-09	-1.86	-11.28	9q33
14	213854_at	SYNGR1	-5.78	9.12E-13	1.70E-09	-1.73	-11.24	22q13.1
15	211991_s_at	HLA-DPA1	-16.03	2.74E-11	1.91E-08	-1.89	-11.05	6p21.3
16	224918_x_at	MGST1	-16.27	1.67E-11	1.40E-08	-1.84	-11.04	12p12.3-p12.1
17	210982_s_at	HLA-DRA	-15.95	3.36E-11	2.09E-08	-1.90	-10.99	6p21.3
18	215193_x_at	HLA-DRB1	-11.40	2.47E-11	1.84E-08	-1.83	-10.91	6p21.3
19	212268_at	SERPINB1	-3.88	2.29E-13	4.66E-10	-1.61	-10.88	6p25
20	238483_at		4.25	2.94E-11	1.93E-08	1.78	10.85	
21	223158_s_at	NEK6	-3.71	1.67E-13	4.16E-10	-1.59	-10.81	9q33.3-q34.11
22	200742_s_at	CLN2	-4.85	2.07E-11	1.61E-08	-1.73	-10.66	11p15
23	206871_at	ELA2	-12.68	3.99E-11	2.29E-08	-1.73	-10.50	19p13.3
24	209312_x_at	HLA-DRB1	-7.10	9.36E-12	8.87E-09	-1.64	-10.49	6p21.3
25	228007_at		6.94	3.02E-10	8.78E-08	1.88	10.45	
26	205418_at	FES	-11.30	2.69E-11	1.91E-08	-1.65	-10.35	15q26.1
27	208894_at	HLA-DRA	-16.69	1.69E-10	6.41E-08	-1.82	-10.30	6p21.3
28	211728_s_at	HYAL3	-7.52	1.41E-10	5.80E-08	-1.70	-10.11	3p21.3
29	231902_at	LOC152485	3.08	1.34E-11	1.20E-08	1.54	10.08	4q31.1
30	208306_x_at	HLA-DRB4	-7.43	3.02E-11	1.93E-08	-1.57	-10.03	6p21.3
31	231736_x_at	MGST1	-16.11	2.20E-10	7.60E-08	-1.72	-10.03	12p12.3-p12.1
32	226878_at		-3.66	2.08E-11	1.61E-08	-1.54	-9.99	
33	206106_at	MAPK12	-4.12	3.54E-12	4.17E-09	-1.48	-9.97	22q13.33
34	223553_s_at	FLJ22570	-4.55	7.46E-11	3.71E-08	-1.59	-9.92	5q35.3
35	202241_at	C8FW	-6.84	1.42E-10	5.80E-08	-1.62	-9.88	8q24.13
36	228827_at		-42.42	5.18E-10	1.28E-07	-1.79	-9.84	
37	225120_at		3.42	2.61E-10	8.00E-08	1.61	9.80	
38	235843_at		-3.56	3.21E-12	3.99E-09	-1.44	-9.78	
39	213572_s_at	SERPINB1	-3.23	1.33E-12	2.29E-09	-1.41	-9.75	6p25
40	223703_at	CDA017	-5.49	5.55E-10	1.34E-07	-1.70	-9.68	10q23.1
41	227979_at		2.53	3.76E-11	2.24E-08	1.48	9.68	
42	200808_s_at	ZYX	-4.91	2.13E-10	7.60E-08	-1.57	-9.63	7q32
43	226178_at		2.42	8.57E-12	8.73E-09	1.42	9.62	

Table 2.1-2.78

44	228345_at		4.86	3.20E-10	9.08E-08	1.55	9.57	
45	221710_x_at	FLJ10647	-6.28	6.12E-11	3.26E-08	-1.47	-9.53	1p34.3
46	218818_at	FHL3	-2.52	9.51E-12	8.87E-09	-1.41	-9.51	1p34
47	218627_at	FLJ11259	-3.13	2.24E-12	3.14E-09	-1.37	-9.50	12q23.3
48	209604_s_at	GATA3	12.98	1.96E-09	3.46E-07	1.73	9.50	10p15
49	222895_s_at	BCL11B	13.16	1.63E-09	3.01E-07	1.67	9.45	14q32.31
50	215706_x_at	ZYX	-4.68	1.94E-10	7.24E-08	-1.50	-9.43	7q32
2.31	ALL_T-lineage versus CLL							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	204670_x_at	HLA-DRB5	-11.20	5.56E-33	1.18E-28	-3.57	-27.19	6p21.3
2	208306_x_at	HLA-DRB4	-13.68	2.45E-31	1.73E-27	-3.45	-26.06	6p21.3
3	209619_at	CD74	-10.94	1.41E-32	1.49E-28	-3.38	-25.90	5q32
4	217478_s_at	HLA-DMA	-18.42	1.59E-24	3.72E-21	-3.45	-23.77	6p21.3
5	209312_x_at	HLA-DRB1	-11.52	1.32E-28	4.66E-25	-3.05	-23.05	6p21.3
6	211990_at	HLA-DPA1	-8.81	2.82E-30	1.49E-26	-2.99	-22.92	6p21.3
7	225927_at		-7.65	7.71E-29	3.26E-25	-2.90	-22.14	
8	215193_x_at	HLA-DRB1	-18.73	2.34E-22	4.50E-19	-2.87	-20.11	6p21.3
9	224838_at	FOXP1	-4.55	2.67E-27	8.06E-24	-2.61	-20.03	3p14.1
10	212827_at	IGHM	-19.11	3.49E-22	6.15E-19	-2.80	-19.72	14q32.33
11	202625_at	LYN	-7.46	7.02E-27	1.85E-23	-2.56	-19.61	8q13
12	208894_at	HLA-DRA	-29.04	2.15E-20	2.17E-17	-2.82	-18.79	6p21.3
13	210982_s_at	HLA-DRA	-29.63	2.29E-20	2.20E-17	-2.78	-18.64	6p21.3
14	203932_at	HLA-DMB	-17.45	9.70E-20	7.32E-17	-2.81	-18.25	6p21.3
15	211991_s_at	HLA-DPA1	-28.13	3.42E-19	2.07E-16	-2.55	-17.15	6p21.3
16	218829_s_at	KIAA1416	-5.05	1.04E-22	2.19E-19	-2.28	-17.15	8q12.1
17	209374_s_at	IGHM	-22.46	2.49E-19	1.69E-16	-2.42	-16.78	14q32.33
18	200999_s_at	CKAP4	-5.61	2.48E-21	3.28E-18	-2.23	-16.60	12q24.11
19	201137_s_at	HLA-DPB1	-13.25	8.43E-20	6.60E-17	-2.32	-16.57	6p21.3
20	226123_at	LOC286180	-6.82	4.35E-22	7.07E-19	-2.16	-16.37	8q12.1
21	243780_at		-18.06	2.55E-19	1.69E-16	-2.27	-16.13	
22	204192_at	CD37	-9.52	1.22E-18	6.28E-16	-2.30	-15.96	19p13-q13.4
23	220987_s_at	SNARK	-7.86	2.99E-18	1.43E-15	-2.32	-15.84	1q32.1
24	202863_at	SP100	-3.99	1.39E-20	1.60E-17	-2.08	-15.55	2q37.1
25	225658_at		-5.69	5.02E-20	4.24E-17	-2.10	-15.54	
26	209306_s_at	SWAP70	-11.40	4.66E-18	2.05E-15	-2.24	-15.45	11p15
27	207132_x_at	PFDN5	-2.30	8.46E-22	1.28E-18	-2.00	-15.37	12q12
28	201417_at		47.61	2.02E-13	1.62E-11	2.83	15.36	
29	223287_s_at	FOXP1	-5.28	5.08E-19	2.83E-16	-2.08	-15.15	3p14.1
30	201029_s_at	CD99	2.99	6.61E-15	8.68E-13	2.31	15.09	Xp22.32
31	227167_s_at		-7.22	6.90E-19	3.74E-16	-2.07	-15.08	
32	204446_s_at	ALOX5	-9.52	3.09E-20	2.84E-17	-2.01	-15.08	10q11.2
33	212386_at		-15.41	9.05E-18	3.54E-15	-2.16	-15.01	
34	229597_s_at	KIAA1607	-7.11	1.61E-19	1.13E-16	-2.02	-14.99	10q11.21

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35	225364_at	LOC200227	-2.88	2.47E-21	3.28E-18	-1.95	-14.97	20q13.11
36	202626_s_at	LYN	-8.70	3.09E-19	1.93E-16	-2.03	-14.96	8q13
37	204613_at	PLCG2	-6.47	1.65E-18	8.30E-16	-2.04	-14.80	16q24.1
38	214786_at	MAP3K1	-9.09	7.59E-18	3.03E-15	-2.07	-14.69	5q11.2
39	209307_at	SWAP70	-9.74	1.34E-17	4.71E-15	-2.08	-14.63	11p15
40	201416_at	SOX4	79.86	7.97E-13	5.21E-11	2.87	14.59	6p22.3
41	218029_at	FLJ13725	-5.84	1.78E-20	1.88E-17	-1.90	-14.51	16q21
42	209075_s_at	NIFU	-2.55	1.44E-20	1.60E-17	-1.89	-14.46	12q24.1
43	218191_s_at	FLJ11240	-2.84	1.37E-20	1.60E-17	-1.87	-14.37	6q12
44	206398_s_at	CD19	-23.31	3.02E-16	6.32E-14	-2.27	-14.30	16p11.2
45	239287_at		-30.92	3.52E-16	7.23E-14	-2.30	-14.26	
46	210754_s_at	LYN	-6.49	1.28E-19	9.36E-17	-1.88	-14.23	8q13
47	213309_at	PLCL2	-8.56	1.20E-17	4.54E-15	-1.98	-14.22	3p24.3
48	200998_s_at	CKAP4	-3.57	4.28E-20	3.77E-17	-1.85	-14.15	12q24.11
49	206337_at	CCR7	-13.34	1.37E-16	3.26E-14	-2.08	-14.12	17q12-q21.2
50	214615_at	P2RY10	-6.52	1.58E-17	5.22E-15	-1.96	-14.08	Xq21.1
2.32	ALL_T-lineage versus CML							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	210254_at	MS4A3	-19.46	1.95E-37	1.83E-33	-3.51	-29.04	11q12
2	206871_at	ELA2	-17.09	1.64E-39	3.08E-35	-3.32	-28.11	19p13.3
3	205557_at	BPI	-16.63	1.16E-36	7.24E-33	-3.27	-27.26	20q11.23-q12
4	203949_at	MPO	-17.81	1.18E-35	4.47E-32	-3.21	-26.66	17q23.1
5	212268_at	SERPINB1	-5.96	2.65E-34	6.21E-31	-2.97	-24.87	6p25
6	206676_at	CEACAM8	-16.46	4.03E-34	8.39E-31	-2.98	-24.79	19q13.2
7	214575_s_at	AZU1	-58.29	2.39E-29	2.03E-26	-3.27	-24.60	19p13.3
8	216379_x_at	KIAA1919	-13.74	1.13E-34	3.54E-31	-2.91	-24.43	6q22
9	209771_x_at	CD24	-12.21	1.19E-35	4.47E-32	-2.88	-24.42	6q21
10	206111_at	RNASE2	-11.53	8.31E-34	1.56E-30	-2.86	-23.92	14q24-q31
11	211657_at	CEACAM6	-16.60	2.61E-31	3.50E-28	-2.94	-23.86	19q13.2
12	212531_at	LCN2	-12.34	2.61E-34	6.21E-31	-2.83	-23.85	9q34
13	210140_at	CST7	-13.66	1.50E-30	1.76E-27	-2.96	-23.73	20p11.21
14	203757_s_at	CEACAM6	-23.78	2.49E-29	2.03E-26	-2.90	-22.99	19q13.2
15	211275_s_at	GYG	-5.82	1.16E-31	1.67E-28	-2.76	-22.85	3q24-q25.1
16	205653_at	CTSG	-23.29	1.03E-28	6.88E-26	-2.84	-22.46	14q11.2
17	204971_at	CSTA	-18.18	8.76E-30	8.21E-27	-2.76	-22.40	3q21
18	201554_x_at	GYG	-7.44	8.37E-31	1.05E-27	-2.71	-22.34	3q24-q25.1
19	208308_s_at	GPI	-5.21	1.15E-32	1.96E-29	-2.64	-22.27	19q13.1
20	203948_s_at	MPO	-28.41	8.93E-29	6.20E-26	-2.77	-22.12	17q23.1
21	203021_at	SLPI	-13.40	5.09E-29	3.82E-26	-2.70	-21.82	20q12
22	204351_at	S100P	-12.62	1.36E-29	1.21E-26	-2.64	-21.59	4p16
23	204174_at	ALOX5AP	-10.76	6.79E-29	4.89E-26	-2.62	-21.31	13q12
24	201061_s_at	STOM	-8.18	4.98E-32	7.78E-29	-2.49	-21.09	9q34.1
25	205513_at	TCN1	-17.05	2.26E-27	1.21E-24	-2.64	-20.95	11q11-q12

Table 2.1-2.78

26	208650_s_at	CD24	-21.33	2.54E-27	1.32E-24	-2.57	-20.58	6q21
27	206851_at	RNASE3	-27.15	5.05E-26	1.93E-23	-2.67	-20.43	14q24-q31
28	219281_at	MSRA	-6.49	6.01E-30	6.26E-27	-2.41	-20.23	8p23.1
29	201858_s_at	PRG1	-6.09	8.67E-27	3.87E-24	-2.46	-20.18	10q22.1
30	201029_s_at	CD99	6.82	1.81E-16	6.14E-15	3.30	20.14	Xp22.32
31	266_s_at	CD24	-16.69	4.09E-27	2.02E-24	-2.47	-19.94	6q21
32	205786_s_at	ITGAM	-9.75	9.43E-28	5.70E-25	-2.42	-19.87	16p11.2
33	209772_s_at	CD24	-39.25	5.08E-25	1.46E-22	-2.65	-19.77	6q21
34	223423_at	GPCR1	-8.72	8.39E-30	8.21E-27	-2.34	-19.74	3q26.2-q27
35	210244_at	CAMP	-26.08	1.21E-25	4.19E-23	-2.54	-19.73	3p21.3
36	200742_s_at	CLN2	-6.32	2.46E-28	1.59E-25	-2.37	-19.67	11p15
37	223120_at	MGC1314	-5.00	4.45E-30	4.90E-27	-2.32	-19.64	6q24
38	200654_at	P4HB	-3.28	1.21E-26	5.27E-24	-2.36	-19.50	17q25
39	207802_at	SGP28	-37.32	6.83E-25	1.88E-22	-2.53	-19.34	6p12.3
40	206207_at	CLC	-30.16	7.93E-25	2.09E-22	-2.53	-19.28	19q13.1
41	221766_s_at	C6orf37	-9.43	6.55E-28	4.09E-25	-2.32	-19.27	6q14
42	205863_at	S100A12	-8.76	4.55E-29	3.56E-26	-2.28	-19.26	1q21
43	208158_s_at	OSBPL1A	-7.11	2.62E-27	1.33E-24	-2.30	-19.02	18q11.1
44	217762_s_at	RAB31	-25.55	3.83E-25	1.16E-22	-2.42	-19.00	18p11.3
45	217764_s_at	RAB31	-16.13	1.12E-24	2.83E-22	-2.38	-18.64	18p11.3
46	206440_at	LIN7A	-21.03	1.39E-24	3.47E-22	-2.38	-18.58	12q21
47	208636_at	ACTN1	-7.90	3.49E-26	1.42E-23	-2.26	-18.53	14q24
48	202391_at	BASP1	-12.43	1.44E-25	4.91E-23	-2.28	-18.45	5p15.1-p14
49	209369_at	ANXA3	-26.20	1.18E-23	2.48E-21	-2.45	-18.34	4q13-q22
50	203936_s_at	MMP9	-13.04	6.50E-25	1.82E-22	-2.28	-18.27	20q11.2-q13.1
2.33	ALL_T-lineage versus normalBM							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	201029_s_at	CD99	4.54	1.49E-16	2.37E-12	2.94	16.60	Xp22.32
2	201858_s_at	PRG1	-5.80	4.79E-12	1.52E-08	-2.93	-15.58	10q22.1
3	218424_s_at	TSAP6	-4.96	1.82E-11	2.88E-08	-2.94	-15.46	2q14.1
4	223280_x_at	MS4A6A	-10.91	2.82E-09	1.06E-06	-3.21	-15.41	11q12.1
5	218257_s_at	UGCGL1	-2.58	2.90E-14	2.30E-10	-2.69	-14.99	2q14.3
6	226190_at		-5.38	3.04E-08	4.91E-06	-3.25	-14.63	
7	210613_s_at	SYNGR1	-6.69	2.88E-10	2.28E-07	-2.78	-14.29	22q13.1
8	202018_s_at	LTF	-5.32	2.64E-11	3.80E-08	-2.66	-14.15	3q21-q23
9	201416_at	SOX4	14.82	2.35E-12	9.30E-09	2.75	13.75	6p22.3
10	203535_at	S100A9	-6.04	4.61E-09	1.36E-06	-2.73	-13.50	1q21
11	201417_at		7.32	1.84E-12	9.30E-09	2.55	13.41	
12	226556_at		-3.16	9.38E-12	1.86E-08	-2.46	-13.37	
13	206488_s_at	CD36	-7.81	1.68E-08	3.28E-06	-2.78	-13.30	7q11.2
14	223120_at	MGC1314	-3.87	7.67E-10	4.49E-07	-2.55	-13.15	6q24
15	224356_x_at	MS4A6A	-11.05	1.24E-07	1.17E-05	-2.88	-12.86	11q12.1
16	222698_s_at	IMPACT	-3.79	1.21E-09	6.59E-07	-2.47	-12.72	18q11.2-q12.1

Table 2.1-2.78

17	212531_at	LCN2	-11.23	5.71E-07	3.14E-05	-2.95	-12.19	9q34
18	221188_s_at	CIDEB	-4.98	3.85E-07	2.49E-05	-2.84	-12.17	14q11.2
19	219013_at	GALNT11	-5.93	1.26E-07	1.18E-05	-2.63	-12.10	7q34-q36
20	208908_s_at	CAST	-6.58	5.78E-08	7.71E-06	-2.49	-11.90	5q15-q21
21	206845_s_at	RNF40	-2.57	6.50E-10	4.12E-07	-2.21	-11.75	16p11.2-p11.1
22	206871_at	ELA2	-16.33	1.09E-06	4.78E-05	-2.94	-11.72	19p13.3
23	200701_at	NPC2	-2.98	2.66E-10	2.22E-07	-2.16	-11.62	14q24.3
24	226448_at		-2.79	1.90E-07	1.54E-05	-2.50	-11.52	
25	201028_s_at	CD99	5.66	1.68E-11	2.88E-08	2.09	11.40	Xp22.32
26	204776_at	THBS4	-5.40	1.05E-06	4.65E-05	-2.75	-11.36	5q13
27	213539_at	CD3D	6.56	7.50E-12	1.86E-08	2.02	11.24	11q23
28	200631_s_at	SET	2.04	8.28E-12	1.86E-08	2.00	11.17	9q34
29	203645_s_at	CD163	-10.25	1.15E-06	4.93E-05	-2.68	-11.16	12p13.3
30	224975_at	NFIA	-4.44	6.27E-07	3.28E-05	-2.51	-11.06	1p31.3-p31.2
31	204393_s_at	ACPP	-4.08	1.19E-07	1.14E-05	-2.28	-10.99	3q21-q23
32	218394_at	FLJ22386	-3.92	1.44E-08	3.04E-06	-2.12	-10.88	16p13.3
33	218739_at	CGI-58	-3.16	6.03E-07	3.20E-05	-2.40	-10.79	3p25.3-p24.3
34	201486_at	RCN2	4.84	1.26E-10	1.27E-07	2.03	10.75	15q23
35	237444_at		-3.98	2.38E-10	2.10E-07	-1.96	-10.75	
36	223664_x_at	BCL2L13	-1.95	1.82E-08	3.50E-06	-2.10	-10.75	22q11
37	223553_s_at	FLJ22570	-5.65	1.71E-06	6.42E-05	-2.59	-10.72	5q35.3
38	214575_s_at	AZU1	-43.05	5.19E-06	1.27E-04	-3.18	-10.58	19p13.3
39	228499_at	PFKFB4	-3.03	5.97E-07	3.20E-05	-2.31	-10.53	3p21-p22
40	201425_at	ALDH2	-4.03	2.91E-09	1.07E-06	-1.97	-10.51	12q24.2
41	236297_at		-3.63	3.70E-07	2.43E-05	-2.19	-10.32	
42	208651_x_at	CD24	-8.81	2.41E-06	7.82E-05	-2.49	-10.31	6q21
43	219304_s_at	SCDGF-B	-2.41	3.55E-08	5.46E-06	-1.99	-10.18	11q22.3
44	201988_s_at	CREBL2	-2.70	9.25E-11	1.05E-07	-1.81	-10.16	12p13
45	228624_at	FLJ11155	-8.45	3.11E-06	9.33E-05	-2.49	-10.14	4q32.1
46	216041_x_at	GRN	-8.03	3.50E-06	1.01E-04	-2.52	-10.12	17q21.32
47	212414_s_at	SEPT6	4.38	4.81E-10	3.17E-07	1.90	10.07	Xq24
48	228716_at		-3.45	4.16E-10	3.14E-07	-1.81	-10.03	
49	205076_s_at	CRA	-3.69	3.51E-06	1.01E-04	-2.46	-10.01	1q12-q21
50	230988_at		-6.14	4.78E-06	1.22E-04	-2.56	-9.98	
2.34	ALL_t(8;14) versus AML_MLL							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	213737_x_at		-6.52	2.80E-19	4.69E-15	-2.31	-15.60	
2	214651_s_at	HOXA9	-41.49	3.25E-16	2.73E-12	-2.48	-15.04	7p15-p14
3	201163_s_at	IGFBP7	-5.53	2.04E-14	8.56E-11	-1.75	-11.75	4q12
4	201105_at	LGALS1	-7.18	1.37E-14	7.66E-11	-1.67	-11.32	22q13.1
5	235753_at		-9.89	1.73E-13	5.80E-10	-1.74	-11.31	
6	209905_at	HOXA9	-225.42	1.97E-12	3.67E-09	-1.90	-11.02	7p15-p14

Table 2.1-2.78

7	201162_at	IGFBP7	-12.89	7.82E-13	1.64E-09	-1.67	-10.80	4q12
8	213147_at	HOXA10	-5.90	3.63E-13	1.01E-09	-1.57	-10.50	7p15-p14
9	228083_at	CACNA2D4	-22.80	6.43E-12	8.04E-09	-1.74	-10.46	12p13.33
10	211709_s_at	SCGF	-11.81	3.27E-12	5.32E-09	-1.64	-10.41	19q13.3
11	214430_at	GLA	-2.65	4.59E-13	1.10E-09	-1.50	-10.13	Xq22
12	202265_at	BMI1	-4.44	6.71E-12	8.04E-09	-1.48	-9.75	10p11.23
13	206847_s_at	HOXA7	-4.83	3.49E-12	5.32E-09	-1.40	-9.50	7p15-p14
14	213150_at	HOXA10	-11.25	6.79E-11	6.15E-08	-1.50	-9.37	7p15-p14
15	221581_s_at	WBSCR5	-3.67	4.92E-12	6.88E-09	-1.38	-9.36	7q11.23
16	204082_at	PBX3	-5.23	2.40E-11	2.37E-08	-1.40	-9.24	9q33-q34
17	204798_at	MYB	-4.22	7.87E-12	8.81E-09	-1.36	-9.23	6q22-q23
18	214875_x_at	APLP2	-3.57	1.00E-11	1.05E-08	-1.35	-9.17	11q24
19	203373_at	SOCS2	-16.27	1.78E-10	1.36E-07	-1.43	-8.99	12q
20	208702_x_at	APLP2	-3.53	1.28E-10	1.02E-07	-1.33	-8.83	11q24
21	215785_s_at	CYFIP2	6.20	4.75E-07	4.09E-05	1.68	8.63	5q34
22	211404_s_at	APLP2	-3.17	2.78E-09	8.80E-07	-1.34	-8.56	11q24
23	203733_at	MYLE	-3.10	6.96E-11	6.15E-08	-1.26	-8.54	16p13.2
24	204168_at	MGST2	-4.41	1.96E-10	1.39E-07	-1.29	-8.53	4q28.3
25	203372_s_at	SOCS2	-20.78	7.83E-10	3.30E-07	-1.39	-8.53	12q
26	201944_at	HEXB	-3.67	1.14E-10	9.58E-08	-1.24	-8.39	5q13
27	212174_at	AK2	-4.10	5.89E-10	2.67E-07	-1.30	-8.38	1p34
28	202546_at	VAMP8	-3.23	2.17E-10	1.46E-07	-1.24	-8.37	2p12-p11.2
29	41220_at	MSF	2.15	1.09E-07	1.35E-05	1.40	8.24	17q25
30	58780_s_at	FLJ10357	-7.09	9.87E-10	3.74E-07	-1.28	-8.23	14q11.1
31	202012_s_at	EXT2	-1.93	1.99E-10	1.39E-07	-1.21	-8.22	11p12-p11
32	223703_at	CDA017	-4.67	2.42E-10	1.46E-07	-1.21	-8.20	10q23.1
33	213908_at		-6.06	2.43E-10	1.46E-07	-1.21	-8.19	
34	209360_s_at	RUNX1	-5.50	2.31E-10	1.46E-07	-1.20	-8.17	21q22.3
35	209605_at	TST	-5.22	4.45E-10	2.34E-07	-1.22	-8.15	22q13.1
36	204069_at	MEIS1	-12.06	1.86E-09	6.42E-07	-1.31	-8.14	2p14-p13
37	224699_s_at	KIAA1228	-3.19	2.82E-10	1.63E-07	-1.20	-8.11	7q36.3
38	219889_at	FRAT1	-2.95	2.98E-10	1.67E-07	-1.20	-8.10	10q24.1
39	206674_at	FLT3	-23.84	2.87E-09	8.93E-07	-1.35	-8.09	13q12
40	213491_x_at	RPN2	-2.29	4.96E-10	2.44E-07	-1.19	-8.01	20q12-q13.1
41	218048_at	BUP	-3.26	1.00E-09	3.74E-07	-1.21	-8.01	10pter-q22.1
42	226676_at	EHZF	-11.62	2.69E-09	8.67E-07	-1.28	-8.00	18q11.1
43	212465_at	FLJ23027	-2.17	4.33E-10	2.34E-07	-1.18	-7.98	14q32.31
44	229838_at	NUCB2	-3.69	5.08E-10	2.44E-07	-1.18	-7.97	11p15.1-p14
45	212442_s_at	LOC253782	-3.72	4.85E-10	2.44E-07	-1.17	-7.96	2q31.1
46	205418_at	FES	-6.91	5.57E-10	2.60E-07	-1.17	-7.92	15q26.1
47	218109_s_at	FLJ14153	-3.05	6.05E-10	2.67E-07	-1.17	-7.91	3q25.32
48	205382_s_at	DF	-9.94	2.02E-09	6.80E-07	-1.21	-7.90	19p13.3
49	225245_x_at	H2AFJ	-3.28	8.26E-10	3.30E-07	-1.17	-7.87	12p12
50	211200_s_at	FGR	-3.87	7.88E-10	3.30E-07	-1.15	-7.81	1p36.2-p36.1

Table 2.1-2.78

2.35	ALL_t(8;14) versus AML_inv(16)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	201029_s_at	CD99	-4.38	3.33E-18	4.82E-14	-3.36	-20.10	Xp22.32
2	200665_s_at	SPARC	-25.46	5.73E-14	1.66E-10	-2.62	-14.63	5q31.3-q32
3	224710_at	RAB34	-7.91	4.29E-15	3.10E-11	-2.11	-13.00	17q11.1
4	203585_at	ZNF185	-3.46	1.45E-14	6.98E-11	-2.12	-12.97	Xq28
5	205382_s_at	DF	-10.80	3.41E-14	1.23E-10	-2.14	-12.92	19p13.3
6	211709_s_at	SCGF	-9.72	2.06E-13	4.96E-10	-2.18	-12.80	19q13.3
7	202747_s_at	ITM2A	-15.81	1.00E-12	1.80E-09	-2.25	-12.73	Xq13.3-Xq21.2
8	202746_at	ITM2A	-9.69	1.66E-12	2.41E-09	-2.10	-12.10	Xq13.3-Xq21.2
9	231982_at		-18.86	1.13E-11	1.18E-08	-2.03	-11.44	
10	215111_s_at	TSC22	-9.09	1.74E-11	1.40E-08	-2.06	-11.42	13q14
11	217989_at	RetSDR2	-3.96	5.65E-11	4.09E-08	-1.93	-11.23	4q21.3
12	209365_s_at	ECM1	-4.48	1.02E-12	1.80E-09	-1.76	-10.79	1q21
13	215116_s_at	DNM1	-13.20	8.05E-11	5.21E-08	-2.00	-10.78	9q34
14	231310_at		-4.90	1.12E-12	1.80E-09	-1.74	-10.73	
15	223471_at	RAB3IP	7.29	9.13E-08	8.36E-06	2.38	10.67	
16	38671_at	KIAA0620	-3.05	2.05E-12	2.70E-09	-1.74	-10.66	3q21.3
17	201497_x_at	MYH11	-11.98	6.27E-11	4.32E-08	-1.78	-10.30	16p13.13-p13.12
18	201564_s_at	FSCN1	-13.17	1.10E-10	5.66E-08	-1.81	-10.25	7p22
19	212667_at	SPARC	-11.41	1.16E-10	5.79E-08	-1.79	-10.19	5q31.3-q32
20	223276_at	NID67	-5.17	7.96E-12	9.61E-09	-1.65	-10.10	5q33.1
21	207075_at	CIAS1	-5.61	1.14E-11	1.18E-08	-1.61	-9.89	1q44
22	203948_s_at	MPO	-4.29	1.74E-09	4.85E-07	-1.72	-9.86	17q23.1
23	220974_x_at	BA108L7.2	-8.57	1.60E-11	1.38E-08	-1.61	-9.85	10q24.31
24	201162_at	IGFBP7	-6.55	1.52E-11	1.38E-08	-1.61	-9.84	4q12
25	203949_at	MPO	-3.54	2.36E-08	3.13E-06	-1.85	-9.83	17q23.1
26	201596_x_at	KRT18	-6.80	9.87E-11	5.36E-08	-1.67	-9.83	12q13
27	225510_at		-4.52	1.62E-11	1.38E-08	-1.57	-9.65	
28	217865_at	GP	-4.38	1.76E-10	7.29E-08	-1.61	-9.64	5q35.3
29	201887_at	IL13RA1	-5.22	1.00E-10	5.36E-08	-1.58	-9.48	Xq24
30	212442_s_at	LOC253782	-4.39	3.92E-11	2.98E-08	-1.53	-9.38	2q31.1
31	208891_at	DUSP6	-5.27	1.21E-10	5.86E-08	-1.53	-9.32	12q22-q23
32	205330_at	MN1	-16.88	1.53E-09	4.35E-07	-1.71	-9.28	22q12.1
33	38487_at	STAB1	-3.60	8.75E-11	5.21E-08	-1.50	-9.21	3p21.31
34	201496_x_at	MYH11	-6.02	8.99E-11	5.21E-08	-1.48	-9.11	16p13.13-p13.12
35	201417_at		-3.29	1.27E-10	5.91E-08	-1.48	-9.09	
36	204044_at	QPRT	-3.86	8.84E-11	5.21E-08	-1.47	-9.06	16p12.1
37	58780_s_at	FLJ10357	-4.92	3.11E-10	1.12E-07	-1.50	-9.03	14q11.1
38	204900_x_at	SAP30	-3.90	2.82E-10	1.05E-07	-1.49	-8.98	4q34.1
39	210613_s_at	SYNGR1	-4.52	1.34E-10	5.95E-08	-1.45	-8.92	22q13.1
40	225831_at	LOC148894	-4.05	1.36E-10	5.95E-08	-1.44	-8.89	1p36.11
41	205131_x_at	SCGF	-12.79	2.39E-09	6.28E-07	-1.56	-8.84	19q13.3
42	201389_at	ITGA5	-3.99	1.73E-10	7.29E-08	-1.43	-8.83	12q11-q13
43	202007_at	NID	-8.75	1.25E-09	3.70E-07	-1.51	-8.82	1q43

Table 2.1-2.78

44	201739_at	SGK	-4.63	2.55E-10	9.98E-08	-1.43	-8.76	6q23
45	214875_x_at	APLP2	-3.35	2.04E-10	8.18E-08	-1.42	-8.74	11q24
46	223095_at	MGC4415	-4.05	2.66E-10	1.01E-07	-1.40	-8.64	10q24.1
47	201015_s_at	JUP	-9.77	9.79E-10	3.15E-07	-1.44	-8.64	17q21
48	206674_at	FLT3	-12.76	5.62E-09	1.13E-06	-1.57	-8.62	13q12
49	208818_s_at	COMT	-3.27	3.98E-10	1.40E-07	-1.40	-8.59	22q11.21
50	209190_s_at	DIAPH1	-2.61	3.63E-09	8.73E-07	-1.44	-8.56	5q31
2.36	ALL_t(8;14) versus AML_inv(3)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	215111_s_at	TSC22	-8.61	1.87E-08	5.11E-05	-2.03	-9.60	13q14
2	38671_at	KIAA0620	-3.21	6.09E-10	1.06E-05	-1.69	-9.30	3q21.3
3	217226_s_at	BA108L7.2	-4.72	5.47E-09	3.18E-05	-1.74	-9.19	10q24.31
4	203746_s_at	HCCS	1.62	1.33E-07	1.13E-04	1.83	8.99	Xp22.3
5	217963_s_at	NGFRAP1	-10.15	3.73E-08	5.11E-05	-1.82	-8.95	Xq22.1
6	201829_at	NET1	-3.60	3.66E-08	5.11E-05	-1.75	-8.78	10p15
7	206295_at	IL18	-8.27	4.38E-08	5.11E-05	-1.71	-8.63	11q22.2-q22.3
8	201029_s_at	CD99	-2.82	2.44E-09	2.13E-05	-1.53	-8.52	Xp22.32
9	224710_at	RAB34	-7.11	2.43E-08	5.11E-05	-1.57	-8.34	17q11.1
10	235199_at		-4.90	2.26E-08	5.11E-05	-1.56	-8.32	
11	229307_at		-5.52	4.26E-08	5.11E-05	-1.60	-8.32	
12	208998_at	UCP2	2.66	1.78E-07	1.24E-04	1.61	8.21	11q13
13	215537_x_at	DDAH2	-6.74	7.77E-08	7.52E-05	-1.59	-8.17	6p21.3
14	217667_at		-3.12	1.68E-08	5.11E-05	-1.43	-7.87	
15	226025_at	KIAA0379	-3.79	2.79E-07	1.67E-04	-1.61	-7.85	3p25.1
16	217989_at	RetSDR2	-3.65	1.16E-08	5.07E-05	-1.41	-7.85	4q21.3
17	226528_at		4.20	5.72E-07	2.65E-04	1.57	7.85	
18	202262_x_at	DDAH2	-4.68	6.77E-08	6.93E-05	-1.45	-7.74	6p21.3
19	231982_at		-26.73	5.80E-07	2.65E-04	-1.68	-7.66	
20	206267_s_at	MATK	-4.19	4.07E-08	5.11E-05	-1.38	-7.60	19p13.3
21	221773_at		-4.69	5.73E-08	6.23E-05	-1.37	-7.51	
22	225799_at	MGC4677	-3.33	4.40E-08	5.11E-05	-1.36	-7.51	2p11.1
23	202371_at	FLJ21174	-5.18	2.50E-07	1.56E-04	-1.44	-7.46	Xq22.1
24	218806_s_at	VAV3	-2.88	4.31E-08	5.11E-05	-1.32	-7.35	1p13.2
25	213504_at	COPS6	2.30	9.52E-07	3.51E-04	1.44	7.34	7q22.1
26	205349_at	GNA15	-6.67	1.39E-07	1.13E-04	-1.35	-7.29	19p13.3
27	212775_at	KIAA0657	-15.19	1.11E-06	3.67E-04	-1.58	-7.28	2q36.1
28	214909_s_at	DDAH2	-5.11	7.13E-07	2.95E-04	-1.46	-7.24	6p21.3
29	210473_s_at	GPR125	-5.49	1.66E-07	1.24E-04	-1.34	-7.22	4p15.31
30	36711_at	MAFF	-9.25	1.09E-06	3.67E-04	-1.51	-7.20	22q13.1
31	225567_at		-5.42	5.93E-07	2.65E-04	-1.40	-7.16	
32	223471_at	RAB3IP	2.62	1.96E-06	4.80E-04	1.43	7.14	
33	226869_at		-7.73	1.74E-07	1.24E-04	-1.28	-7.03	
34	220974_x_at	BA108L7.2	-6.98	3.13E-07	1.70E-04	-1.30	-7.01	10q24.31

Table 2.1-2.78

35	202747_s_at	ITM2A	-9.26	1.29E-06	4.08E-04	-1.43	-7.01	Xq13.3-Xq21.2
36	217870_s_at	UMP-CMPK	-1.89	2.97E-07	1.67E-04	-1.30	-6.99	
37	220668_s_at	DNMT3B	-4.04	6.99E-07	2.95E-04	-1.35	-6.99	20q11.2
38	201938_at	CDK2AP1	-2.01	1.36E-07	1.13E-04	-1.26	-6.97	12q24.31
39	206995_x_at	SCARF1	-3.46	5.92E-07	2.65E-04	-1.32	-6.96	17p13.3
40	228252_at	PIF1	4.11	9.45E-06	1.14E-03	1.57	6.94	15q22.1
41	218899_s_at	BAALC	-14.83	2.21E-06	5.03E-04	-1.52	-6.93	8q22.3
42	206478_at	KIAA0125	-9.64	1.90E-06	4.73E-04	-1.45	-6.91	14q32.33
43	204897_at	PTGER4	-2.97	1.43E-07	1.13E-04	-1.24	-6.90	5p13.1
44	38340_at	HIP1R	2.64	3.89E-06	6.72E-04	1.39	6.86	12q24
45	211181_x_at		-3.62	2.97E-07	1.67E-04	-1.25	-6.86	
46	225306_s_at	C14orf69	-3.90	3.51E-07	1.80E-04	-1.25	-6.83	14q32.32
47	204446_s_at	ALOX5	3.52	7.09E-07	2.95E-04	1.26	6.79	10q11.2
48	223708_at	C1QTNF4	-47.84	3.17E-06	5.82E-04	-1.55	-6.78	11q11
49	212235_at	KIAA0620	-3.58	2.01E-07	1.35E-04	-1.22	-6.78	3q21.3
50	217975_at	LOC51186	-7.72	2.52E-06	5.28E-04	-1.39	-6.73	Xq22.1
2.37	ALL_t(8;14) versus AML_komplext							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	212293_at	Nbak2	-2.65	2.17E-12	6.91E-08	-1.43	-9.72	1p12
2	201548_s_at	PLU-1	-3.44	3.81E-11	1.73E-07	-1.45	-9.62	1q32.1
3	213737_x_at		-4.14	7.58E-12	8.05E-08	-1.38	-9.37	
4	212397_at	RDX	-3.33	5.30E-12	8.05E-08	-1.37	-9.36	11q23
5	219201_s_at	TWSG1	-9.58	3.02E-11	1.60E-07	-1.43	-9.34	18p11.3
6	202265_at	BMI1	-4.19	1.52E-11	9.67E-08	-1.40	-9.32	10p11.23
7	206015_s_at	KIAA1041	-2.30	1.30E-11	9.67E-08	-1.32	-9.03	1pter-q31.3
8	214651_s_at	HOXA9	-22.40	3.19E-10	5.09E-07	-1.42	-8.77	7p15-p14
9	201807_at	VPS26	-2.44	3.71E-10	5.60E-07	-1.32	-8.73	10q21.1
10	201829_at	NET1	-3.31	2.02E-10	4.95E-07	-1.30	-8.58	10p15
11	215111_s_at	TSC22	-7.00	4.76E-10	5.71E-07	-1.34	-8.53	13q14
12	205791_x_at	ZNF230	-4.47	8.54E-11	3.40E-07	-1.24	-8.47	19q13.31
13	202747_s_at	ITM2A	-9.76	3.87E-10	5.60E-07	-1.30	-8.45	Xq13.3-Xq21.2
14	222182_s_at	CNOT2	-2.14	1.68E-10	4.86E-07	-1.25	-8.43	12q14.3
15	201994_at	MORF4L2	-1.74	9.95E-10	7.93E-07	-1.26	-8.35	Xq22
16	201029_s_at	CD99	-2.95	1.19E-10	3.80E-07	-1.22	-8.33	Xp22.32
17	203519_s_at	UPF2	-2.12	1.19E-10	3.80E-07	-1.21	-8.32	10p14-p13
18	218649_x_at	SDCCAG1	-2.04	4.04E-10	5.60E-07	-1.23	-8.31	14q22
19	206175_x_at	ZNF222	-6.74	3.17E-10	5.09E-07	-1.24	-8.28	19q13.2
20	201196_s_at	AMD1	-1.94	3.05E-10	5.09E-07	-1.21	-8.25	6q21-q22
21	218280_x_at	HIST2H2AA	-4.51	2.55E-10	5.09E-07	-1.21	-8.21	1q21.2
22	226869_at		-13.19	4.50E-10	5.71E-07	-1.23	-8.20	
23	45687_at	MGC3121	-2.08	1.94E-10	4.95E-07	-1.19	-8.17	16p11.2
24	207643_s_at	TNFRSF1A	-5.26	2.39E-10	5.09E-07	-1.18	-8.12	12p13.2
25	214290_s_at	HIST2H2AA	-3.83	2.64E-10	5.09E-07	-1.18	-8.11	1q21.2

Table 2.1-2.78

26	200677_at	PTTG1IP	-3.00	2.82E-10	5.09E-07	-1.18	-8.09	21q22.3
27	217963_s_at	NGFRAP1	-8.45	1.17E-09	9.06E-07	-1.24	-8.09	Xq22.1
28	202746_at	ITM2A	-6.30	8.80E-10	7.38E-07	-1.22	-8.06	Xq13.3-Xq21.2
29	38671_at	KIAA0620	-2.68	4.62E-10	5.71E-07	-1.18	-8.03	3q21.3
30	218618_s_at	FAD104	-4.31	6.84E-10	6.60E-07	-1.19	-8.01	3q26.31
31	219793_at	SNX16	-2.98	6.74E-10	6.60E-07	-1.19	-8.00	8q21.12
32	208634_s_at	MACF1	-3.96	7.71E-10	7.06E-07	-1.19	-7.98	1p32-p31
33	213074_at		-2.98	8.01E-10	7.06E-07	-1.19	-7.97	
34	201263_at	TARS	-2.29	5.51E-10	6.22E-07	-1.16	-7.95	5p13.2
35	201325_s_at	EMP1	-25.32	3.24E-09	1.62E-06	-1.29	-7.94	12p12.3
36	218718_at	PDGFC	-8.17	2.42E-09	1.38E-06	-1.24	-7.93	4q32
37	201920_at	SLC20A1	-2.21	4.84E-10	5.71E-07	-1.16	-7.92	2q11-q14
38	201324_at	EMP1	-15.80	3.59E-09	1.74E-06	-1.28	-7.90	12p12.3
39	204798_at	MYB	-3.91	6.05E-10	6.22E-07	-1.15	-7.86	6q22-q23
40	227481_at	FLJ31349	-4.17	6.03E-10	6.22E-07	-1.15	-7.85	6q25.2
41	201830_s_at	NET1	-3.93	5.89E-10	6.22E-07	-1.15	-7.85	10p15
42	200929_at	TMP21	-2.13	1.20E-09	9.11E-07	-1.15	-7.79	14q24.3
43	214700_x_at	DKFZP434D193	-2.83	7.94E-10	7.06E-07	-1.13	-7.77	2q23.3
44	217523_at	CD44	-4.18	8.20E-10	7.06E-07	-1.13	-7.76	11p13
45	209160_at	AKR1C3	-14.63	5.61E-09	2.35E-06	-1.25	-7.74	10p15-p14
46	202797_at	SACM1L	-2.78	9.05E-10	7.39E-07	-1.13	-7.73	3p21.3
47	209905_at	HOXA9	-90.93	6.69E-09	2.56E-06	-1.30	-7.72	7p15-p14
48	226545_at		-6.01	2.60E-09	1.38E-06	-1.15	-7.65	
49	201604_s_at	PPP1R12A	-2.28	1.53E-09	1.12E-06	-1.12	-7.64	12q15-q21
50	210613_s_at	SYNGR1	-5.32	1.54E-09	1.12E-06	-1.12	-7.61	22q13.1
2.38	ALL_t(8;14) versus AML_t(15;17)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	201029_s_at	CD99	-5.10	1.50E-19	2.05E-15	-3.57	-20.49	Xp22.32
2	205382_s_at	DF	-23.02	1.94E-15	5.31E-12	-3.72	-19.69	19p13.3
3	221004_s_at	ITM2C	-23.37	1.41E-14	2.42E-11	-3.48	-18.24	2q37
4	214450_at	CTSW	-28.11	7.12E-14	1.08E-10	-3.39	-17.43	11q13.1
5	212953_x_at	CALR	-4.79	1.17E-14	2.28E-11	-3.24	-17.39	19p13.3-p13.2
6	38487_at	STAB1	-28.53	4.42E-13	5.03E-10	-3.47	-16.84	3p21.31
7	203948_s_at	MPO	-7.72	1.26E-16	8.64E-13	-2.93	-16.74	17q23.1
8	224918_x_at	MGST1	-5.83	3.58E-16	1.63E-12	-2.70	-15.53	12p12.3-p12.1
9	211709_s_at	SCGF	-14.81	7.77E-13	7.59E-10	-2.92	-15.16	19q13.3
10	231736_x_at	MGST1	-6.39	1.68E-15	5.31E-12	-2.65	-15.13	12p12.3-p12.1
11	208689_s_at	RPN2	-2.72	2.65E-15	6.03E-12	-2.61	-14.94	20q12-q13.1
12	205624_at	CPA3	-22.18	5.59E-12	3.49E-09	-2.88	-14.35	3q21-q25
13	201825_s_at	CGI-49	-5.55	2.72E-12	2.06E-09	-2.61	-13.81	1q44
14	203949_at	MPO	-4.67	1.52E-11	8.01E-09	-2.46	-13.25	17q23.1
15	200654_at	P4HB	-3.40	9.86E-13	8.42E-10	-2.33	-13.04	17q25
16	208852_s_at	CANX	-3.48	5.36E-13	5.63E-10	-2.20	-12.46	5q35

Table 2.1-2.78

17	212509_s_at		-12.77	6.52E-11	2.55E-08	-2.48	-12.45	
18	219869_s_at	BIGM103	-4.34	3.24E-12	2.33E-09	-2.25	-12.41	4q22-q24
19	213854_at	SYNGR1	-4.61	2.03E-13	2.78E-10	-2.14	-12.30	22q13.1
20	205349_at	GNA15	-8.27	3.03E-13	3.77E-10	-2.12	-12.13	19p13.3
21	238365_s_at		-12.76	1.66E-11	8.41E-09	-2.21	-12.00	
22	238022_at		-7.91	8.42E-13	7.67E-10	-2.11	-11.99	
23	204150_at	STAB1	-31.21	3.01E-10	8.75E-08	-2.50	-11.80	3p21.31
24	201028_s_at	CD99	-8.53	2.61E-10	7.93E-08	-2.31	-11.54	Xp22.32
25	201596_x_at	KRT18	-17.74	3.94E-10	1.06E-07	-2.34	-11.44	12q13
26	210613_s_at	SYNGR1	-7.36	8.22E-12	4.88E-09	-2.04	-11.43	22q13.1
27	213491_x_at	RPN2	-2.41	1.42E-11	7.75E-09	-2.03	-11.40	20q12-q13.1
28	217716_s_at	SEC61A1	-2.53	2.15E-12	1.73E-09	-1.95	-11.22	3q21.3
29	231982_at		-19.65	3.57E-10	1.02E-07	-2.20	-11.18	
30	221739_at	IL27w	-2.27	2.69E-11	1.23E-08	-2.00	-11.18	19p13.3
31	222477_s_at	TM7SF3	-5.40	2.15E-10	7.01E-08	-2.11	-11.08	12q11-q12
32	204347_at	AK3	-7.50	9.46E-12	5.39E-09	-1.95	-11.05	1p31.3
33	217225_x_at	LOC283820	-2.34	4.91E-12	3.36E-09	-1.88	-10.82	16p13.13
34	228543_at	CSRP2BP	2.66	3.98E-10	1.06E-07	1.99	10.81	20p11.23
35	209215_at	TETRAN	-4.32	5.61E-12	3.49E-09	-1.87	-10.75	4p16.3
36	215116_s_at	DNM1	-13.38	1.31E-09	2.57E-07	-2.20	-10.70	9q34
37	242520_s_at		-15.81	4.04E-10	1.06E-07	-1.97	-10.51	
38	208675_s_at	DDOST	-2.73	2.23E-11	1.09E-08	-1.83	-10.44	1p36.1
39	45687_at	MGC3121	-2.54	4.98E-11	2.00E-08	-1.86	-10.43	16p11.2
40	200986_at	SERPING1	-12.30	7.27E-10	1.69E-07	-1.99	-10.43	11q12-q13.1
41	202012_s_at	EXT2	-3.31	6.81E-10	1.60E-07	-1.98	-10.40	11p12-p11
42	206761_at	TACTILE	-13.70	1.87E-09	3.39E-07	-2.09	-10.37	3q13.13
43	202262_x_at	DDAH2	-5.99	1.48E-10	5.18E-08	-1.85	-10.25	6p21.3
44	214575_s_at	AZU1	-6.54	2.62E-11	1.23E-08	-1.79	-10.24	19p13.3
45	213399_x_at	RPN2	-2.25	3.55E-11	1.57E-08	-1.78	-10.19	20q12-q13.1
46	201826_s_at	CGI-49	-3.82	1.08E-09	2.20E-07	-1.94	-10.18	1q44
47	201162_at	IGFBP7	-9.47	6.34E-10	1.52E-07	-1.86	-10.04	4q12
48	220987_s_at	SNARK	4.66	6.39E-08	5.74E-06	2.09	10.03	1q32.1
49	210788_s_at	retSDR4	-3.07	4.49E-11	1.86E-08	-1.74	-9.98	14q22.3
50	200656_s_at	P4HB	-5.21	5.45E-10	1.38E-07	-1.83	-9.97	17q25
2.39	ALL_t(8;14) versus AML_t(8;21)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	211709_s_at	SCGF	-11.39	6.95E-14	1.15E-09	-2.35	-13.68	19q13.3
2	209160_at	AKR1C3	-12.54	1.29E-11	4.28E-08	-2.05	-11.47	10p15-p14
3	203949_at	MPO	-4.28	2.82E-11	5.85E-08	-1.82	-10.80	17q23.1
4	210613_s_at	SYNGR1	-7.40	6.49E-12	2.70E-08	-1.75	-10.54	22q13.1
5	203948_s_at	MPO	-5.64	3.20E-12	2.65E-08	-1.68	-10.32	17q23.1
6	217989_at	RetSDR2	-3.72	2.87E-10	2.97E-07	-1.75	-10.21	4q21.3
7	213854_at	SYNGR1	-4.63	6.53E-12	2.70E-08	-1.66	-10.16	22q13.1

Table 2.1-2.78

8	218718_at	PDGFC	-8.39	1.59E-10	1.76E-07	-1.77	-10.05	4q32
9	201825_s_at	CGI-49	-4.35	1.05E-10	1.58E-07	-1.74	-10.04	1q44
10	201029_s_at	CD99	-3.99	2.17E-11	5.14E-08	-1.64	-9.93	Xp22.32
11	38671_at	KIAA0620	-2.85	2.11E-11	5.14E-08	-1.61	-9.82	3q21.3
12	228827_at		-29.89	6.68E-10	5.34E-07	-1.85	-9.77	
13	209122_at	ADFP	-3.27	4.96E-11	9.12E-08	-1.54	-9.42	9p21.3
14	206940_s_at	POU4F1	-32.15	1.62E-09	1.03E-06	-1.82	-9.38	13q21.1-q22
15	212133_at	MGC5466	2.43	4.32E-08	1.04E-05	1.71	9.20	15q11.2
16	228058_at	LOC124220	-5.47	5.51E-11	9.12E-08	-1.49	-9.20	16p13.3
17	212229_s_at	FBXO21	3.50	7.06E-10	5.34E-07	1.54	9.16	12q24.22
18	232232_s_at	CT2	-4.04	1.34E-10	1.71E-07	-1.47	-9.00	6q22.1
19	209318_x_at	PLAGL1	-3.96	1.30E-10	1.71E-07	-1.46	-8.95	6q24-q25
20	201015_s_at	JUP	-11.06	7.40E-10	5.34E-07	-1.50	-8.90	17q21
21	202012_s_at	EXT2	-1.91	1.54E-10	1.76E-07	-1.43	-8.84	11p12-p11
22	220987_s_at	SNARK	3.24	3.05E-07	4.21E-05	1.76	8.80	1q32.1
23	224710_at	RAB34	-7.15	5.01E-10	4.61E-07	-1.46	-8.78	17q11.1
24	222477_s_at	TM7SF3	-3.98	1.40E-09	9.26E-07	-1.49	-8.76	12q11-q12
25	215537_x_at	DDAH2	-5.24	4.30E-10	4.19E-07	-1.44	-8.75	6p21.3
26	212442_s_at	LOC253782	-4.56	7.41E-10	5.34E-07	-1.39	-8.49	2q31.1
27	211341_at	POU4F1	-83.12	1.12E-08	4.30E-06	-1.66	-8.47	13q21.1-q22
28	235353_at	KIAA0746	4.67	1.10E-06	1.06E-04	1.83	8.44	4p15.2
29	219869_s_at	BIGM103	-2.34	7.21E-10	5.34E-07	-1.37	-8.41	4q22-q24
30	201826_s_at	CGI-49	-3.67	6.17E-09	2.76E-06	-1.48	-8.40	1q44
31	231982_at		-20.00	1.07E-08	4.30E-06	-1.53	-8.35	
32	205528_s_at	CBFA2T1	-23.20	1.58E-08	5.44E-06	-1.54	-8.24	8q22
33	221004_s_at	ITM2C	-6.92	2.18E-09	1.24E-06	-1.35	-8.16	2q37
34	202262_x_at	DDAH2	-3.60	1.18E-09	8.17E-07	-1.32	-8.15	6p21.3
35	210473_s_at	GPR125	-6.10	2.18E-09	1.24E-06	-1.34	-8.12	4p15.31
36	212231_at	FBXO21	3.26	1.95E-07	3.02E-05	1.47	8.05	12q24.22
37	205382_s_at	DF	-12.14	1.53E-08	5.44E-06	-1.41	-8.02	19p13.3
38	201723_s_at	GALNT1	-1.81	1.75E-09	1.07E-06	-1.30	-7.99	18q12.1
39	211728_s_at	HYAL3	-3.62	5.14E-09	2.57E-06	-1.31	-7.91	3p21.3
40	206761_at	TACTILE	-9.40	3.47E-08	9.36E-06	-1.41	-7.79	3q13.13
41	204548_at	STAR	-17.83	4.39E-08	1.04E-05	-1.44	-7.76	8p11.2
42	213355_at	ST3GALVI	-4.80	3.92E-09	2.16E-06	-1.26	-7.75	3q12.1
43	225306_s_at	C14orf69	-6.91	2.28E-08	7.34E-06	-1.34	-7.74	14q32.32
44	203859_s_at	PALM	-4.37	5.27E-09	2.57E-06	-1.27	-7.73	19p13.3
45	205529_s_at	CBFA2T1	-6.28	1.11E-08	4.30E-06	-1.29	-7.72	8q22
46	224833_at	ETS1	6.68	2.27E-06	1.83E-04	1.61	7.71	11q23.3
47	201564_s_at	FSCN1	-11.83	3.96E-08	1.01E-05	-1.38	-7.69	7p22
48	211474_s_at	SERPINB6	-3.41	4.54E-09	2.42E-06	-1.25	-7.69	6p25
49	204798_at	MYB	-3.76	5.92E-09	2.76E-06	-1.26	-7.68	6q22-q23
50	201028_s_at	CD99	-5.30	4.12E-08	1.03E-05	-1.37	-7.66	Xp22.32
2.40	ALL_t(8;14) versus CLL							

Table 2.1-2.78

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	225927_at		-2.74	3.75E-18	5.46E-14	-2.12	-14.68	
2	239287_at		-11.04	9.76E-16	2.03E-12	-1.96	-13.08	
3	218191_s_at	FLJ11240	-2.41	2.75E-16	1.00E-12	-1.87	-12.96	6q12
4	227670_at	ZNF75A	-4.28	9.20E-17	6.69E-13	-1.81	-12.69	16p13.11
5	217906_at	KLHDC2	-2.06	3.98E-15	4.82E-12	-1.84	-12.59	14q21.3
6	225629_s_at	KIAA1538	-4.65	2.18E-16	1.00E-12	-1.79	-12.48	17p13.1
7	205105_at	MAN2A1	-2.74	7.99E-16	2.03E-12	-1.77	-12.29	5q21-q22
8	212589_at	RRAS2	-5.94	8.38E-16	2.03E-12	-1.70	-11.93	11p15.2
9	214615_at	P2RY10	-4.21	1.37E-15	2.50E-12	-1.69	-11.78	Xq21.1
10	217478_s_at	HLA-DMA	-2.79	6.67E-14	3.88E-11	-1.73	-11.75	6p21.3
11	226508_at		-3.07	1.83E-15	2.95E-12	-1.67	-11.71	
12	213295_at		-3.01	3.34E-15	4.65E-12	-1.68	-11.70	
13	224709_s_at	SPEC2	-2.40	4.03E-12	8.03E-10	-1.75	-11.47	5q31.1
14	206337_at	CCR7	-6.16	3.52E-15	4.65E-12	-1.64	-11.46	17q12-q21.2
15	39582_at		-3.38	5.11E-14	3.23E-11	-1.66	-11.38	
16	208306_x_at	HLA-DRB4	-2.43	9.66E-12	1.43E-09	-1.75	-11.37	6p21.3
17	205997_at	ADAM28	-28.23	8.14E-14	4.08E-11	-1.71	-11.36	8p21.1
18	218149_s_at	DKFZp434K1210	-3.46	1.09E-14	1.21E-11	-1.62	-11.30	8p21.1
19	230689_at		-9.61	7.93E-14	4.08E-11	-1.66	-11.19	
20	224838_at	FOXP1	-3.09	5.53E-10	3.68E-08	-1.85	-11.17	3p14.1
21	221718_s_at	AKAP13	-2.20	7.28E-14	4.07E-11	-1.62	-11.16	15q24-q25
22	236280_at		-4.68	1.70E-14	1.76E-11	-1.58	-11.02	
23	226538_at		-2.97	3.16E-14	2.56E-11	-1.57	-10.95	
24	213034_at	KIAA0999	-3.12	2.20E-14	1.89E-11	-1.57	-10.94	11q23.3
25	205933_at	SETBP1	-7.67	3.86E-14	2.86E-11	-1.58	-10.94	18q21.1
26	205788_s_at	KIAA0663	-1.81	2.19E-14	1.89E-11	-1.56	-10.89	1q32.1
27	207700_s_at	NCOA3	-4.18	2.20E-14	1.89E-11	-1.56	-10.89	20q12
28	207132_x_at	PFDN5	-2.18	1.74E-10	1.47E-08	-1.71	-10.78	12q12
29	217952_x_at	PHF3	-2.18	1.76E-13	7.37E-11	-1.55	-10.73	
30	213142_x_at	LOC54103	-5.50	4.82E-14	3.19E-11	-1.54	-10.72	7q11.23
31	212959_s_at	MGC4170	-4.15	4.23E-14	2.93E-11	-1.53	-10.69	12q23.3
32	203057_s_at	PRDM2	-3.21	3.94E-14	2.86E-11	-1.53	-10.68	1p36
33	202880_s_at	PSCD1	-2.64	4.19E-12	8.24E-10	-1.59	-10.67	17q25
34	209061_at	SULF2	-3.66	5.92E-14	3.59E-11	-1.52	-10.63	20q12-13.2
35	212590_at	RRAS2	-4.05	2.24E-13	8.59E-11	-1.53	-10.60	11p15.2
36	208456_s_at	RRAS2	-5.30	2.08E-13	8.19E-11	-1.53	-10.59	11p15.2
37	41660_at	CELSR1	-10.17	3.14E-13	1.06E-10	-1.54	-10.50	22q13.3
38	202254_at	KIAA0440	-8.20	5.16E-13	1.53E-10	-1.56	-10.49	14q24.1
39	212914_at	PKP4	-10.57	4.16E-13	1.32E-10	-1.55	-10.49	2q23-q31
40	213567_at		-2.79	1.28E-13	6.01E-11	-1.51	-10.48	
41	226869_at		-10.28	8.06E-14	4.08E-11	-1.50	-10.47	
42	229844_at		-3.51	1.96E-13	7.92E-11	-1.51	-10.46	
43	212569_at	KIAA0650	-3.18	1.39E-13	6.14E-11	-1.49	-10.41	18p11.31
44	209236_at	SLC23A1	-4.55	9.73E-14	4.72E-11	-1.48	-10.39	20p13

Table 2.1-2.78

45	205192_at	MAP3K14	-3.14	2.97E-13	1.03E-10	-1.48	-10.31	17q21
46	212614_at	MRF2	-5.02	4.76E-13	1.44E-10	-1.51	-10.31	10q22.1
47	236226_at		-6.96	1.33E-13	6.03E-11	-1.48	-10.31	
48	230245_s_at	LOC283663	-15.22	3.00E-12	6.33E-10	-1.62	-10.30	15q21.2
49	204882_at	KIAA0053	-7.94	9.56E-13	2.48E-10	-1.52	-10.25	2p13.2
50	AFFX-HUMGAPDH/M33197_3_at - HG-U133B	GAPD	1.91	2.46E-10	1.95E-08	1.60	10.22	12p13
2.41	ALL_t(8;14) versus CML							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	231982_at		-15.81	5.94E-23	1.12E-18	-2.05	-16.03	
2	214575_s_at	AZU1	-7.93	3.75E-15	5.07E-12	-1.95	-14.19	19p13.3
3	208158_s_at	OSBPL1A	-4.40	2.89E-16	6.82E-13	-1.76	-13.26	18q11.1
4	205653_at	CTSG	-5.64	2.09E-14	1.88E-11	-1.78	-13.00	14q11.2
5	209485_s_at	OSBPL1A	-8.61	1.81E-18	1.71E-14	-1.63	-12.77	18q11.1
6	210140_at	CST7	-4.40	3.97E-13	1.63E-10	-1.76	-12.60	20p11.21
7	204669_s_at	RNF24	-7.19	5.55E-15	6.56E-12	-1.68	-12.56	20p13-p12.1
8	201904_s_at	HYA22	-8.42	3.20E-17	1.51E-13	-1.61	-12.51	3p21.3
9	225386_s_at	LOC92906	-5.00	4.00E-12	9.32E-10	-1.78	-12.38	2p22.2
10	207949_s_at	ICA1	-5.20	2.66E-16	6.82E-13	-1.60	-12.30	7p22
11	228497_at	FLIPT1	-5.91	4.78E-18	3.01E-14	-1.56	-12.30	1p13.1
12	202794_at	INPP1	-3.18	2.53E-15	3.98E-12	-1.55	-11.83	2q32
13	203948_s_at	MPO	-5.15	3.07E-12	8.16E-10	-1.63	-11.64	17q23.1
14	213572_s_at	SERPINB1	-3.87	1.16E-09	9.03E-08	-1.87	-11.62	6p25
15	213541_s_at	ERG	-5.55	5.94E-17	2.24E-13	-1.47	-11.59	21q22.3
16	200654_at	P4HB	-2.85	1.11E-09	8.71E-08	-1.85	-11.54	17q25
17	211709_s_at	SCGF	-7.05	8.05E-17	2.54E-13	-1.47	-11.54	19q13.3
18	201825_s_at	CGI-49	-2.70	8.44E-16	1.59E-12	-1.49	-11.53	1q44
19	226869_at		-8.85	5.19E-14	3.63E-11	-1.52	-11.44	
20	225782_at	LOC253827	-5.40	2.54E-13	1.12E-10	-1.54	-11.41	12q14.1
21	217989_at	RetSDR2	-4.11	5.20E-12	1.18E-09	-1.60	-11.40	4q21.3
22	203949_at	MPO	-4.10	2.75E-10	2.87E-08	-1.73	-11.38	17q23.1
23	205769_at	SLC27A2	-4.79	4.23E-16	8.87E-13	-1.45	-11.33	15q21.2
24	219010_at	FLJ10901	-4.29	1.27E-13	7.08E-11	-1.50	-11.21	1q31.3
25	201905_s_at	HYA22	-5.12	9.89E-13	3.49E-10	-1.53	-11.19	3p21.3
26	222692_s_at	FAD104	-4.20	7.67E-15	8.05E-12	-1.45	-11.17	3q26.31
27	210613_s_at	SYNGR1	-4.39	1.75E-11	3.12E-09	-1.58	-11.11	22q13.1
28	214430_at	GLA	-2.20	1.22E-12	4.03E-10	-1.52	-11.11	Xq22
29	228726_at		-4.69	4.55E-14	3.30E-11	-1.43	-10.91	
30	213737_x_at		-3.56	9.17E-10	7.46E-08	-1.65	-10.79	
31	219890_at	CLECSF5	-6.04	1.96E-15	3.36E-12	-1.36	-10.71	7q33
32	202441_at	KEO4	-3.16	3.58E-11	5.52E-09	-1.52	-10.70	10q21-q22
33	208636_at	ACTN1	-4.82	3.14E-11	4.99E-09	-1.51	-10.69	14q24

Table 2.1-2.78

34	204798_at	MYB	-4.11	8.56E-15	8.51E-12	-1.37	-10.64	6q22-q23
35	218618_s_at	FAD104	-3.81	4.77E-15	6.00E-12	-1.35	-10.58	3q26.31
36	206207_at	CLC	-4.67	3.39E-12	8.55E-10	-1.44	-10.56	19q13.1
37	209215_at	TETRAN	-3.99	1.83E-13	8.41E-11	-1.39	-10.56	4p16.3
38	211728_s_at	HYAL3	-4.14	2.90E-15	4.21E-12	-1.34	-10.53	3p21.3
39	207341_at	PRTN3	-8.55	6.24E-15	6.93E-12	-1.35	-10.51	19p13.3
40	205768_s_at	SLC27A2	-4.51	3.47E-14	2.63E-11	-1.34	-10.41	15q21.2
41	203675_at	NUCB2	-4.04	3.36E-10	3.35E-08	-1.51	-10.36	11p15.1-p14
42	226794_at	STXBP5	-4.13	8.68E-14	5.47E-11	-1.34	-10.33	6q24.3
43	217963_s_at	NGFRAP1	-5.76	1.58E-14	1.49E-11	-1.28	-10.08	Xq22.1
44	239213_at	SERPINB1	-5.74	3.21E-14	2.58E-11	-1.28	-10.05	6p25
45	208637_x_at	ACTN1	-5.34	1.04E-10	1.29E-08	-1.41	-10.05	14q24
46	218251_at	STRAIT11499	-3.47	1.12E-13	6.41E-11	-1.30	-10.05	Xp11.4
47	206871_at	ELA2	-3.91	1.89E-08	8.88E-07	-1.66	-10.04	19p13.3
48	204381_at	LRP3	-6.49	3.96E-11	5.90E-09	-1.39	-10.02	19q13.11
49	212268_at	SERPINB1	-4.01	5.05E-08	1.97E-06	-1.76	-10.01	6p25
50	205471_s_at	DACH	-4.66	1.66E-13	8.06E-11	-1.29	-10.00	13q22
2.42	ALL_t(8;14) versus normalBM							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	209160_at	AKR1C3	-9.54	1.37E-06	3.29E-03	-2.94	-11.16	10p15-p14
2	210613_s_at	SYNGR1	-4.68	9.89E-10	3.16E-05	-2.32	-10.86	22q13.1
3	218718_at	PDGFC	-3.27	2.04E-07	1.64E-03	-1.85	-8.48	4q32
4	226751_at	DKFZP566K1924	-5.01	5.51E-06	5.40E-03	-2.03	-8.36	2p13.2
5	217047_s_at	FAM13A1	-2.86	7.28E-08	1.16E-03	-1.77	-8.29	4q22.1
6	232232_s_at	CT2	-4.92	2.30E-06	3.87E-03	-1.90	-8.24	6q22.1
7	226806_s_at		-3.83	3.82E-06	4.91E-03	-1.88	-8.04	
8	223437_at	MGC2452	-3.69	6.53E-07	2.08E-03	-1.72	-7.87	22q13.31
9	205051_s_at	KIT	-3.79	2.06E-07	1.64E-03	-1.65	-7.72	4q11-q12
10	203645_s_at	CD163	-4.45	5.86E-07	2.08E-03	-1.66	-7.66	12p13.3
11	222078_at	HCN3	-5.52	2.99E-05	1.02E-02	-1.99	-7.62	1q21.3
12	206488_s_at	CD36	-3.06	3.02E-07	1.93E-03	-1.61	-7.53	7q11.2
13	218424_s_at	TSAP6	-2.56	5.25E-07	2.08E-03	-1.62	-7.48	2q14.1
14	202973_x_at	FAM13A1	-2.99	3.98E-07	2.08E-03	-1.60	-7.47	4q22.1
15	214575_s_at	AZU1	-5.85	2.07E-06	3.87E-03	-1.64	-7.40	19p13.3
16	227627_at	SGKL	-3.18	5.78E-07	2.08E-03	-1.57	-7.34	8q12.3-8q13.1
17	223044_at	SLC11A3	-4.21	9.69E-07	2.81E-03	-1.58	-7.31	2q32
18	209605_at	TST	-3.60	2.84E-06	4.12E-03	-1.63	-7.31	22q13.1
19	223769_x_at	HT036	-2.62	1.42E-06	3.29E-03	-1.59	-7.24	1p34.1
20	226608_at	SAS10	2.81	4.94E-06	5.12E-03	1.67	7.18	4q13.3
21	230988_at		-3.45	3.35E-06	4.65E-03	-1.57	-7.09	
22	209048_s_at	PRKCBP1	-2.10	1.15E-05	7.30E-03	-1.61	-7.00	20q13.12
23	206871_at	ELA2	-3.74	1.60E-06	3.29E-03	-1.49	-6.92	19p13.3
24	208152_s_at	DDX21	1.66	2.26E-06	3.87E-03	1.50	6.89	10q21

Table 2.1-2.78

25	213056_at	KIAA1013	-2.36	1.60E-06	3.29E-03	-1.47	-6.84	3p14.1
26	204976_s_at	AMMECR1	-2.47	7.48E-06	6.29E-03	-1.53	-6.82	Xq22.3
27	213292_s_at	SNX13	-1.97	2.71E-06	4.12E-03	-1.48	-6.82	7p21.1
28	208158_s_at	OSBPL1A	-3.32	1.13E-05	7.30E-03	-1.52	-6.72	18q11.1
29	226590_at	LOC286334	-2.76	1.65E-06	3.29E-03	-1.43	-6.69	9q32
30	222624_s_at	LOC51193	2.36	2.82E-06	4.12E-03	1.45	6.69	3q27.1
31	202616_s_at	MECP2	-3.12	4.43E-06	5.05E-03	-1.42	-6.56	Xq28
32	218247_s_at	LOC51320	2.79	7.37E-06	6.29E-03	1.45	6.50	18q21.1
33	227230_s_at	KIAA1211	-4.05	5.57E-06	5.40E-03	-1.39	-6.42	4q12
34	213012_at	NEDD4	-3.29	1.62E-05	8.46E-03	-1.44	-6.41	15q
35	210140_at	CST7	-3.93	3.02E-05	1.02E-02	-1.47	-6.38	20p11.21
36	205927_s_at	CTSE	-3.69	2.18E-05	9.52E-03	-1.45	-6.38	1q31
37	225437_s_at	MGC22916	2.34	8.17E-06	6.52E-03	1.40	6.34	7p22.3
38	218729_at	LXN	-2.87	7.14E-05	1.44E-02	-1.55	-6.34	3q25.32
39	213541_s_at	ERG	-5.93	1.48E-04	2.05E-02	-1.70	-6.33	21q22.3
40	223166_x_at	FLJ10101	1.66	3.87E-06	4.91E-03	1.35	6.33	9q34.3
41	226869_at		-6.29	1.24E-05	7.50E-03	-1.39	-6.31	
42	204776_at	THBS4	-2.69	4.31E-06	5.05E-03	-1.35	-6.30	5q13
43	217963_s_at	NGFRAP1	-4.26	5.10E-05	1.31E-02	-1.49	-6.30	Xq22.1
44	202061_s_at	SEL1L	-2.06	4.70E-06	5.12E-03	-1.35	-6.29	14q24.3-q31
45	201432_at	CAT	-2.21	4.00E-06	4.91E-03	-1.34	-6.27	11p13
46	219714_s_at	CACNA2D3	-5.89	3.01E-05	1.02E-02	-1.41	-6.20	3p21.1
47	203506_s_at	TNRC11	-1.81	4.97E-06	5.12E-03	-1.32	-6.20	Xq13
48	212628_at		-2.29	6.43E-05	1.40E-02	-1.47	-6.18	
49	203100_s_at	CDYL	-2.57	1.30E-05	7.66E-03	-1.35	-6.16	6p25.1
50	225202_at	RHOBTB3	-2.04	9.34E-06	6.78E-03	-1.34	-6.14	5q14.3
2.43	AML_MLL versus AML_inv(16)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	213737_x_at		3.65	1.30E-18	3.71E-14	2.17	15.48	
2	214651_s_at	HOXA9	22.10	4.22E-16	6.01E-12	2.26	14.60	7p15-p14
3	200665_s_at	SPARC	-14.82	7.41E-14	3.52E-10	-2.27	-14.07	5q31.3-q32
4	200953_s_at	CCND2	-4.16	1.61E-15	1.53E-11	-1.86	-13.20	12p13
5	202746_at	ITM2A	-16.05	9.80E-13	2.15E-09	-2.15	-12.88	Xq13.3-Xq21.2
6	202747_s_at	ITM2A	-16.65	8.69E-13	2.06E-09	-2.09	-12.76	Xq13.3-Xq21.2
7	235753_at		14.15	1.49E-13	6.06E-10	1.98	12.10	
8	227567_at		5.31	5.68E-15	4.05E-11	1.66	11.93	
9	229215_at	ASCL2	11.42	2.22E-13	6.34E-10	1.73	11.48	11p15.5
10	206847_s_at	HOXA7	7.10	2.07E-13	6.34E-10	1.70	11.41	7p15-p14
11	231310_at		-4.40	2.33E-14	1.33E-10	-1.54	-11.24	
12	201497_x_at	MYH11	-27.86	4.74E-11	4.22E-08	-2.16	-11.23	16p13.13-p13.12
13	200951_s_at	CCND2	-4.96	2.30E-12	4.22E-09	-1.60	-10.90	12p13
14	209905_at	HOXA9	70.38	2.46E-12	4.22E-09	1.82	10.90	7p15-p14
15	224049_at	KCNK17	-4.35	2.74E-11	2.70E-08	-1.66	-10.60	6p21.1

Table 2.1-2.78

16	213147_at	HOXA10	5.72	2.97E-13	7.68E-10	1.48	10.56	7p15-p14
17	203949_at	MPO	-3.36	1.91E-13	6.34E-10	-1.41	-10.32	17q23.1
18	213908_at		15.52	8.76E-12	9.99E-09	1.66	10.30	
19	201496_x_at	MYH11	-6.20	5.40E-11	4.67E-08	-1.56	-10.14	16p13.13-p13.12
20	202370_s_at	CBFB	3.09	3.66E-12	5.22E-09	1.46	10.07	16q22.1
21	202931_x_at	BIN1	-3.16	1.41E-12	2.87E-09	-1.39	-10.05	2q14
22	226517_at	BCAT1	-10.55	1.85E-10	1.15E-07	-1.66	-10.05	12pter-q12
23	204082_at	PBX3	5.42	2.57E-11	2.61E-08	1.52	9.76	9q33-q34
24	212667_at	SPARC	-7.96	2.45E-10	1.42E-07	-1.54	-9.70	5q31.3-q32
25	225831_at	LOC148894	-3.79	5.89E-11	4.89E-08	-1.41	-9.59	1p36.11
26	203733_at	MYLE	3.27	3.18E-12	5.03E-09	1.30	9.50	16p13.2
27	223385_at	CYP2S1	-2.38	1.24E-10	8.39E-08	-1.38	-9.34	19q13.1
28	205330_at	MN1	-16.74	1.73E-09	5.37E-07	-1.75	-9.33	22q12.1
29	223471_at	RAB3IP	3.58	7.10E-12	8.43E-09	1.28	9.29	
30	201830_s_at	NET1	-4.44	3.73E-10	2.00E-07	-1.42	-9.26	10p15
31	202551_s_at	CRIM1	-4.62	2.91E-10	1.63E-07	-1.39	-9.23	2p21
32	210139_s_at	PMP22	-9.69	1.47E-09	4.81E-07	-1.55	-9.18	17p12-p11.2
33	224772_at	NAV1	-2.82	3.27E-10	1.79E-07	-1.37	-9.12	
34	211012_s_at	PML	-2.69	1.13E-11	1.24E-08	-1.24	-9.09	15q22
35	228058_at	LOC124220	-5.16	4.73E-12	6.12E-09	-1.22	-9.09	16p13.3
36	223299_at	LOC90701	2.79	4.18E-12	5.67E-09	1.20	9.00	18q21.31
37	214452_at	BCAT1	-4.30	3.97E-10	2.02E-07	-1.34	-8.99	12pter-q12
38	228497_at	FLIPT1	7.80	2.17E-10	1.29E-07	1.41	8.98	1p13.1
39	225102_at	LOC152009	5.25	8.41E-11	6.48E-08	1.30	8.95	3q21.3
40	201828_x_at	CXX1	2.85	2.52E-12	4.22E-09	1.17	8.91	Xq26
41	203948_s_at	MPO	-3.51	6.09E-12	7.55E-09	-1.19	-8.91	17q23.1
42	200602_at	APP	-6.96	1.09E-10	7.70E-08	-1.26	-8.90	21q21.3
43	218041_x_at	SLC38A2	-1.65	3.59E-12	5.22E-09	-1.17	-8.90	12q
44	225285_at		-9.24	1.04E-09	3.97E-07	-1.35	-8.82	
45	203373_at	SOCS2	13.18	2.48E-10	1.42E-07	1.34	8.82	12q
46	201029_s_at	CD99	-1.85	1.78E-11	1.88E-08	-1.18	-8.75	Xp22.32
47	213150_at	HOXA10	8.63	1.06E-10	7.70E-08	1.25	8.74	7p15-p14
48	228496_s_at	CRIM1	-2.68	8.74E-11	6.56E-08	-1.20	-8.70	2p21
49	221581_s_at	WBSCR5	2.78	3.22E-11	3.06E-08	1.19	8.70	7q11.23
50	205453_at	HOXB2	-6.83	3.79E-10	2.00E-07	-1.25	-8.69	17q21-q22
2.44	AML_MLL versus AML_inv(3)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	204082_at	PBX3	8.60	2.88E-12	2.35E-08	1.63	10.50	9q33-q34
2	226789_at		3.28	1.48E-13	1.81E-09	1.47	10.39	
3	214651_s_at	HOXA9	4.67	9.43E-14	1.81E-09	1.45	10.29	7p15-p14
4	235753_at		4.92	3.97E-12	2.43E-08	1.42	9.76	
5	228083_at	CACNA2D4	11.16	1.43E-11	5.83E-08	1.46	9.66	12p13.33
6	214643_x_at	BIN1	-4.56	2.50E-09	1.64E-06	-1.59	-9.58	2q14

Table 2.1-2.78

7	209905_at	HOXA9	7.79	3.17E-11	1.11E-07	1.34	9.13	7p15-p14
8	202054_s_at	ALDH3A2	5.02	6.40E-12	3.14E-08	1.27	9.05	17p11.2
9	208116_s_at	MAN1A1	-4.86	2.19E-08	6.38E-06	-1.59	-8.95	6q22
10	236398_s_at		5.77	7.08E-11	1.58E-07	1.31	8.88	
11	201829_at	NET1	-3.59	3.90E-08	9.18E-06	-1.61	-8.81	10p15
12	203733_at	MYLE	2.69	6.75E-11	1.58E-07	1.23	8.59	16p13.2
13	212318_at	TRN-SR	2.53	8.52E-11	1.67E-07	1.23	8.55	7q32.2
14	233955_x_at	HSPC195	-4.61	1.78E-08	5.60E-06	-1.41	-8.54	5q31.3
15	213893_x_at	PMS2L5	2.24	3.81E-11	1.17E-07	1.19	8.49	7q11-q22
16	208702_x_at	APLP2	2.83	4.39E-11	1.19E-07	1.19	8.45	11q24
17	231431_s_at		-2.62	7.32E-08	1.39E-05	-1.54	-8.45	
18	202605_at	GUSB	3.28	9.55E-11	1.67E-07	1.20	8.44	7q21.11
19	210006_at	DKFZP564O243	2.17	1.66E-10	2.71E-07	1.21	8.40	3p21.1
20	210201_x_at	BIN1	-2.98	1.82E-08	5.64E-06	-1.35	-8.34	2q14
21	214439_x_at	BIN1	-3.31	1.27E-08	4.55E-06	-1.31	-8.27	2q14
22	212782_x_at	POLR2J	2.38	3.41E-10	4.29E-07	1.18	8.24	7q11.2
23	200602_at	APP	-10.57	8.51E-08	1.58E-05	-1.47	-8.24	21q21.3
24	214875_x_at	APLP2	2.72	9.39E-11	1.67E-07	1.15	8.23	11q24
25	219551_at	TRAITS	3.35	3.68E-10	4.29E-07	1.19	8.19	3q13.33
26	206847_s_at	HOXA7	2.98	2.37E-10	3.23E-07	1.16	8.15	7p15-p14
27	218217_at	RISC	4.10	1.13E-09	9.89E-07	1.23	8.14	17q23.1
28	223703_at	CDA017	3.49	1.23E-09	1.00E-06	1.22	8.09	10q23.1
29	201186_at	LRPAP1	3.21	7.48E-10	7.89E-07	1.18	8.07	4p16.3
30	201105_at	LGALS1	2.91	1.88E-10	2.88E-07	1.12	8.00	22q13.1
31	203725_at	GADD45A	-3.08	1.71E-09	1.27E-06	-1.16	-7.99	1p31.2-p31.1
32	214430_at	GLA	2.03	2.27E-10	3.23E-07	1.12	7.97	Xq22
33	206440_at	LIN7A	8.55	1.13E-09	9.89E-07	1.17	7.97	12q21
34	211709_s_at	SCGF	4.44	4.41E-10	4.91E-07	1.11	7.86	19q13.3
35	219033_at	FLJ21308	3.62	1.20E-09	1.00E-06	1.14	7.85	5q11.1
36	219126_at	XAP135	1.85	3.53E-10	4.29E-07	1.10	7.84	6q27
37	208967_s_at	AK2	3.68	3.22E-09	1.84E-06	1.20	7.83	1p34
38	212174_at	AK2	3.63	1.63E-09	1.24E-06	1.15	7.83	1p34
39	202053_s_at	ALDH3A2	2.61	9.28E-10	8.75E-07	1.11	7.78	17p11.2
40	202961_s_at	ATP5J2	2.16	8.60E-10	8.43E-07	1.10	7.77	7q22.1
41	201830_s_at	NET1	-5.62	3.42E-07	3.90E-05	-1.47	-7.75	10p15
42	231300_at	LOC90835	4.14	2.74E-09	1.68E-06	1.15	7.74	16p11.2
43	204951_at	ARHH	-3.59	3.51E-08	8.51E-06	-1.21	-7.71	4p13
44	211404_s_at	APLP2	2.23	1.44E-09	1.14E-06	1.09	7.65	11q24
45	219991_at	SLC2A9	2.29	2.55E-09	1.64E-06	1.12	7.64	4p16-p15.3
46	223328_at	MGC3195	2.12	7.73E-10	7.89E-07	1.07	7.61	7q22.1
47	213908_at		3.56	4.03E-09	2.10E-06	1.12	7.58	
48	228652_at	FLJ38288	-2.21	6.80E-08	1.32E-05	-1.21	-7.58	19q13.43
49	214953_s_at	APP	-5.50	1.23E-07	1.99E-05	-1.23	-7.52	21q21.3
50	202931_x_at	BIN1	-3.09	1.11E-07	1.89E-05	-1.21	-7.50	2q14

Table 2.1-2.78

2.45	AML_MLL versus AML_komplext							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	201377_at	NICE-4	-2.72	3.69E-15	2.46E-11	-1.51	-11.56	1q21.3
2	201105_at	LGALS1	4.52	6.07E-14	2.57E-10	1.36	10.55	22q13.1
3	200608_s_at	RAD21	-1.86	3.88E-15	2.46E-11	-1.28	-10.40	8q24
4	228083_at	CACNA2D4	11.81	1.68E-11	9.93E-09	1.53	9.94	12p13.33
5	201830_s_at	NET1	-5.21	6.70E-12	6.55E-09	-1.37	-9.77	10p15
6	201225_s_at	SRRM1	-1.72	1.39E-13	4.42E-10	-1.18	-9.52	1p36.11
7	208886_at	H1F0	-7.16	2.03E-11	9.93E-09	-1.32	-9.40	22q13.1
8	214700_x_at	DKFZP434D193	-3.12	1.37E-11	9.65E-09	-1.27	-9.33	2q23.3
9	209022_at	STAG2	-1.98	3.31E-12	5.25E-09	-1.17	-9.17	Xq25
10	218041_x_at	SLC38A2	-1.84	3.42E-13	8.70E-10	-1.12	-9.13	12q
11	203544_s_at	STAM	-4.39	3.49E-11	1.48E-08	-1.26	-9.11	10p14-p13
12	218823_s_at	FLJ20038	-2.77	3.12E-11	1.41E-08	-1.25	-9.09	8p21.1
13	201196_s_at	AMD1	-1.93	1.72E-12	3.49E-09	-1.14	-9.09	6q21-q22
14	201560_at	CLIC4	-4.16	4.61E-12	5.33E-09	-1.16	-9.07	1p36.11
15	202746_at	ITM2A	-10.44	1.47E-10	3.83E-08	-1.28	-8.85	Xq13.3-Xq21.2
16	209705_at		-2.03	1.78E-11	9.93E-09	-1.14	-8.80	
17	205788_s_at	KIAA0663	-1.79	1.87E-11	9.93E-09	-1.14	-8.78	1q32.1
18	203519_s_at	UPF2	-2.09	1.91E-11	9.93E-09	-1.13	-8.75	10p14-p13
19	222902_s_at	FLJ21144	-1.92	1.92E-12	3.49E-09	-1.08	-8.75	1p34.1
20	233168_s_at	IMAGE3510317	-1.73	4.52E-12	5.33E-09	-1.09	-8.75	22q13.33
21	209362_at	SURB7	-2.15	1.91E-11	9.93E-09	-1.11	-8.67	12p11.23
22	204082_at	PBX3	4.49	5.32E-11	2.05E-08	1.14	8.66	9q33-q34
23	201585_s_at	SFPQ	-1.91	9.60E-12	8.21E-09	-1.09	-8.65	1p34.3
24	200997_at	RBM4	-1.92	1.18E-11	8.79E-09	-1.09	-8.64	11q13
25	201829_at	NET1	-3.30	1.95E-10	4.21E-08	-1.21	-8.62	10p15
26	239071_at		-1.83	3.72E-12	5.25E-09	-1.04	-8.51	
27	203725_at	GADD45A	-4.33	6.08E-11	2.21E-08	-1.11	-8.51	1p31.2-p31.1
28	211137_s_at	ATP2C1	-3.12	4.82E-10	7.28E-08	-1.26	-8.50	3q21-q24
29	202747_s_at	ITM2A	-10.27	3.18E-10	5.61E-08	-1.20	-8.49	Xq13.3-Xq21.2
30	201166_s_at	PUM1	-1.86	3.89E-11	1.60E-08	-1.09	-8.49	1p35.2
31	212232_at	FNBP4	-1.77	1.15E-11	8.79E-09	-1.05	-8.43	11p11.12
32	200086_s_at - HG-U133B	COX4I1	1.64	5.17E-12	5.47E-09	1.03	8.43	16q22-qter
33	223318_s_at	MGC10974	3.61	2.44E-10	4.77E-08	1.14	8.38	19p13.3
34	212463_at		-4.10	1.52E-10	3.83E-08	-1.11	-8.35	
35	213549_at	PRO2730	-4.66	6.44E-10	8.52E-08	-1.21	-8.33	3p21.31
36	201358_s_at	COPB	-1.65	1.96E-11	9.93E-09	-1.04	-8.33	11p15.2
37	212031_at	S164	-2.00	1.55E-11	9.93E-09	-1.03	-8.32	14q24.3
38	228974_at		-4.54	1.70E-10	4.01E-08	-1.10	-8.31	
39	205849_s_at	UQCRB	1.52	9.70E-12	8.21E-09	1.02	8.31	8q22
40	201061_s_at	STOM	-3.25	2.69E-10	5.17E-08	-1.12	-8.31	9q34.1
41	205639_at	AOAH	3.94	2.96E-10	5.43E-08	1.12	8.29	7p14-p12
42	218331_s_at	FLJ20360	-2.05	6.54E-11	2.31E-08	-1.06	-8.28	10p15.1

Table 2.1-2.78

43	223592_s_at	MGC13061	2.62	2.99E-10	5.43E-08	1.12	8.28	17q11.2
44	217887_s_at	EPS15	-2.10	5.29E-11	2.05E-08	-1.05	-8.26	1p32
45	200985_s_at	CD59	-4.95	1.95E-10	4.21E-08	-1.09	-8.25	11p13
46	214439_x_at	BIN1	-3.72	2.41E-10	4.77E-08	-1.09	-8.21	2q14
47	200071_at - HG-U133A	SPF30	-1.69	7.53E-11	2.52E-08	-1.04	-8.19	10q23
48	202413_s_at	USP1	-1.73	3.43E-11	1.48E-08	-1.01	-8.16	1p32.1-p31.3
49	218846_at	CRSP3	-2.57	3.67E-10	6.13E-08	-1.09	-8.15	6q22.33-q24.1
50	202659_at	PSMB10	3.04	1.05E-10	3.27E-08	1.04	8.15	16q22.1
2.46	AML_MLL versus AML_t(15;17)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	221004_s_at	ITM2C	-9.69	6.96E-15	2.78E-11	-2.63	-16.45	2q37
2	38487_at	STAB1	-16.22	3.38E-13	4.51E-10	-2.90	-16.13	3p21.31
3	203948_s_at	MPO	-6.32	8.76E-21	2.10E-16	-2.19	-15.83	17q23.1
4	214651_s_at	HOXA9	237.17	2.30E-16	1.84E-12	2.66	15.41	7p15-p14
5	205624_at	CPA3	-36.02	6.17E-12	3.79E-09	-3.01	-14.75	3q21-q25
6	212953_x_at	CALR	-3.21	2.50E-14	6.66E-11	-2.22	-14.41	19p13.3-p13.2
7	214450_at	CTSW	-6.11	7.04E-14	1.41E-10	-2.21	-14.15	11q13.1
8	203949_at	MPO	-4.43	9.42E-19	1.13E-14	-1.91	-13.87	17q23.1
9	200953_s_at	CCND2	-6.10	3.06E-12	2.45E-09	-2.26	-13.42	12p13
10	213147_at	HOXA10	23.93	1.62E-14	4.85E-11	2.12	13.06	7p15-p14
11	238022_at		-5.73	4.14E-12	3.00E-09	-1.96	-12.30	
12	235753_at		16.83	1.12E-13	1.79E-10	2.04	12.26	
13	233072_at	KIAA1857	-11.75	7.57E-11	2.44E-08	-2.24	-12.25	9q34
14	205771_s_at	AKAP7	10.25	3.35E-14	8.02E-11	1.82	12.10	6q23
15	206871_at	ELA2	-3.69	4.90E-16	2.94E-12	-1.64	-11.89	19p13.3
16	206847_s_at	HOXA7	9.48	6.90E-14	1.41E-10	1.80	11.89	7p15-p14
17	209448_at	HTATIP2	10.38	2.48E-13	3.64E-10	1.79	11.54	11p15.1
18	204150_at	STAB1	-19.25	3.63E-10	8.30E-08	-2.23	-11.50	3p21.31
19	213587_s_at	LOC155066	7.64	6.58E-13	7.88E-10	1.79	11.29	7q36.1
20	205663_at	PCBP3	-3.93	3.63E-11	1.36E-08	-1.79	-11.19	21q22.3
21	201522_x_at	SNRPN	4.63	2.51E-15	1.20E-11	1.54	11.19	15q12
22	212509_s_at		-6.33	1.53E-10	4.37E-08	-1.87	-11.08	
23	209905_at	HOXA9	720.22	1.83E-12	1.75E-09	1.92	11.06	7p15-p14
24	205349_at	GNA15	-4.14	1.47E-12	1.53E-09	-1.62	-11.03	19p13.3
25	200951_s_at	CCND2	-6.76	2.21E-10	5.88E-08	-1.88	-10.98	12p13
26	206761_at	TACTILE	-28.74	1.21E-09	2.02E-07	-2.29	-10.90	3q13.13
27	201029_s_at	CD99	-2.16	1.08E-14	3.69E-11	-1.48	-10.74	Xp22.32
28	217848_s_at	PP	3.89	1.09E-13	1.79E-10	1.49	10.59	10q11.1-q24
29	225532_at	LOC91768	-5.64	9.02E-10	1.64E-07	-1.92	-10.59	18q11.1
30	200952_s_at	CCND2	-4.07	2.77E-10	6.83E-08	-1.76	-10.57	12p13
31	204425_at	ARHGAP4	15.58	4.11E-12	3.00E-09	1.65	10.49	Xq28
32	204082_at	PBX3	8.50	2.90E-12	2.40E-09	1.61	10.47	9q33-q34

Table 2.1-2.78

33	231736_x_at	MGST1	-2.80	2.58E-13	3.64E-10	-1.46	-10.42	12p12.3-p12.1
34	210788_s_at	retSDR4	-2.38	2.11E-11	9.75E-09	-1.57	-10.41	14q22.3
35	224918_x_at	MGST1	-2.62	9.12E-14	1.68E-10	-1.42	-10.30	12p12.3-p12.1
36	201596_x_at	KRT18	-8.14	5.16E-10	1.08E-07	-1.69	-10.20	12q13
37	213150_at	HOXA10	45.69	1.41E-11	7.20E-09	1.71	10.17	7p15-p14
38	218404_at	SNX10	6.77	5.71E-12	3.60E-09	1.53	10.09	7p15.2
39	225386_s_at	LOC92906	34.47	1.65E-11	8.20E-09	1.66	10.08	2p22.2
40	211474_s_at	SERPINB6	4.55	2.77E-12	2.40E-09	1.47	10.04	6p25
41	221253_s_at	MGC3178	-2.99	2.44E-10	6.44E-08	-1.59	-10.03	6p24.3
42	228083_at	CACNA2D4	11.77	1.68E-11	8.20E-09	1.57	9.93	12p13.33
43	213571_s_at	EIF4EL3	2.54	6.08E-13	7.67E-10	1.37	9.84	2q37.1
44	208852_s_at	CANX	-2.26	6.45E-11	2.18E-08	-1.46	-9.78	5q35
45	227999_at	LOC170394	3.11	7.06E-13	8.06E-10	1.36	9.76	10q26.3
46	217716_s_at	SEC61A1	-1.93	1.04E-11	5.68E-09	-1.40	-9.72	3q21.3
47	202265_at	BMI1	4.29	8.23E-12	4.70E-09	1.43	9.71	10p11.23
48	217853_at	TEM6	6.43	1.19E-11	6.31E-09	1.43	9.66	7p15.1
49	223663_at	FLJ37970	6.99	2.35E-12	2.17E-09	1.37	9.66	11q12.3
50	228263_at	GRASP	-2.66	3.59E-12	2.77E-09	-1.36	-9.63	12q13.13
2.47	AML_MLL versus AML_t(8;21)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	214651_s_at	HOXA9	207.35	2.33E-16	6.38E-12	2.65	15.40	7p15-p14
2	221581_s_at	WBSCR5	10.61	3.46E-15	2.36E-11	2.04	13.41	7q11.23
3	213147_at	HOXA10	17.19	2.21E-14	1.01E-10	2.00	12.78	7p15-p14
4	235753_at		15.72	1.24E-13	4.83E-10	2.01	12.20	
5	201105_at	LGALS1	7.06	3.40E-15	2.36E-11	1.63	11.87	22q13.1
6	206847_s_at	HOXA7	7.80	1.77E-13	6.06E-10	1.79	11.69	7p15-p14
7	227853_at		3.59	7.38E-15	4.04E-11	1.54	11.33	
8	203949_at	MPO	-4.06	7.26E-16	9.92E-12	-1.47	-11.16	17q23.1
9	209905_at	HOXA9	687.57	1.83E-12	4.55E-09	1.92	11.06	7p15-p14
10	213908_at		16.07	8.41E-12	1.53E-08	1.68	10.33	
11	213150_at	HOXA10	58.80	1.26E-11	2.16E-08	1.73	10.23	7p15-p14
12	210314_x_at	TNFSF13	4.81	5.81E-13	1.59E-09	1.42	10.22	17p13.1
13	228827_at		-110.08	4.44E-10	2.89E-07	-1.99	-10.05	
14	228083_at	CACNA2D4	12.77	1.51E-11	2.29E-08	1.60	10.05	12p13.33
15	209500_x_at	TNFSF13	4.18	3.77E-12	7.93E-09	1.39	9.82	17p13.1
16	204082_at	PBX3	6.63	5.42E-12	1.06E-08	1.39	9.77	9q33-q34
17	228058_at	LOC124220	-6.07	2.57E-12	5.84E-09	-1.33	-9.70	16p13.3
18	203948_s_at	MPO	-4.62	4.25E-13	1.29E-09	-1.28	-9.66	17q23.1
19	206940_s_at	POU4F1	-41.89	1.43E-09	6.02E-07	-1.86	-9.46	13q21.1-q22
20	212423_at	FLJ90798	5.26	1.45E-11	2.29E-08	1.34	9.42	10q22.3
21	201944_at	HEXB	3.49	5.23E-11	5.29E-08	1.44	9.41	5q13
22	223562_at	PARVG	3.11	2.14E-11	2.67E-08	1.34	9.35	22q13.2-q13

Table 2.1-2.78

23	229406_at		-12.04	2.06E-09	7.54E-07	-1.65	-9.19	
24	205639_at	AOAH	5.75	2.05E-11	2.67E-08	1.29	9.18	7p14-p12
25	204202_at	KIAA1023	3.45	2.15E-11	2.67E-08	1.28	9.13	7p22.3
26	205529_s_at	CBFA2T1	-12.90	2.76E-09	8.88E-07	-1.70	-9.10	8q22
27	230650_at		-5.19	2.41E-09	8.23E-07	-1.55	-9.01	
28	206009_at	ITGA9	-3.49	2.03E-10	1.50E-07	-1.30	-8.95	3p21.3
29	203859_s_at	PALM	-5.31	1.28E-09	5.66E-07	-1.39	-8.88	19p13.3
30	217853_at	TEM6	5.32	2.90E-11	3.44E-08	1.22	8.87	7p15.1
31	201850_at	CAPG	8.40	4.01E-10	2.67E-07	1.37	8.73	2cen-q24
32	224415_s_at	HINT2	1.98	1.84E-11	2.65E-08	1.16	8.66	9p13.1
33	216417_x_at	HOXB9	3.56	3.49E-11	3.81E-08	1.17	8.64	17q21.3
34	203733_at	MYLE	2.65	6.93E-11	6.53E-08	1.18	8.59	16p13.2
35	211341_at	POU4F1	-266.20	9.63E-09	2.23E-06	-1.69	-8.54	13q21.1-q22
36	225245_x_at	H2AFJ	4.56	3.12E-11	3.55E-08	1.15	8.54	12p12
37	204069_at	MEIS1	20.28	8.95E-10	4.51E-07	1.42	8.54	2p14-p13
38	205528_s_at	CBFA2T1	-41.63	1.17E-08	2.56E-06	-1.63	-8.45	8q22
39	206761_at	TACTILE	-19.71	1.31E-08	2.72E-06	-1.57	-8.38	3q13.13
40	204880_at	MGMT	-2.31	1.57E-10	1.26E-07	-1.14	-8.36	10q26
41	225386_s_at	LOC92906	7.38	1.95E-10	1.48E-07	1.15	8.31	2p22.2
42	225009_at	CKLFSF4	4.99	6.86E-10	3.83E-07	1.22	8.29	16q21
43	202746_at	ITM2A	-6.60	3.24E-09	9.84E-07	-1.25	-8.28	Xq13.3-Xq21.2
44	218217_at	RISC	4.76	3.65E-10	2.49E-07	1.17	8.28	17q23.1
45	232227_at		-11.48	1.52E-08	2.99E-06	-1.50	-8.27	
46	238756_at		3.91	6.11E-10	3.55E-07	1.20	8.26	
47	224301_x_at	H2AFJ	3.97	1.00E-10	8.64E-08	1.11	8.24	12p12
48	212459_x_at	SUCLG2	3.21	4.89E-11	5.14E-08	1.09	8.21	3p14.2
49	241706_at	LOC144402	6.44	1.09E-09	5.31E-07	1.19	8.13	12q11
50	225344_at	ERAP140	-4.28	9.94E-09	2.25E-06	-1.30	-8.13	6q22.33
2.48	AML_MLL versus CLL							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	224838_at	FOXP1	-6.07	8.36E-29	6.94E-25	-3.56	-26.98	3p14.1
2	41220_at	MSF	-3.19	8.08E-33	1.34E-28	-2.71	-22.48	17q25
3	202880_s_at	PSCD1	-6.55	4.92E-24	1.36E-20	-2.70	-20.46	17q25
4	225927_at		-4.22	6.07E-27	3.36E-23	-2.41	-19.51	
5	212827_at	IGHM	-17.91	8.69E-23	1.23E-19	-2.55	-19.23	14q32.33
6	223514_at	CARD11	-41.15	3.94E-20	1.87E-17	-2.91	-18.90	7p22
7	224837_at	FOXP1	-3.88	9.76E-22	8.11E-19	-2.51	-18.62	3p14.1
8	201163_s_at	IGFBP7	35.15	9.25E-19	2.36E-16	2.92	18.36	4q12
9	207168_s_at	H2AFY	3.01	1.91E-24	6.35E-21	2.23	17.97	5q31.3-q32
10	226905_at		7.02	3.02E-25	1.25E-21	2.21	17.94	
11	204215_at	MGC4175	-5.22	2.93E-22	2.72E-19	-2.30	-17.78	7q21.1-q21.2
12	224833_at	ETS1	-10.03	2.95E-22	2.72E-19	-2.29	-17.73	11q23.3

Table 2.1-2.78

13	204951_at	ARHH	-14.78	6.87E-20	2.85E-17	-2.53	-17.71	4p13
14	243780_at		-37.44	6.73E-19	1.93E-16	-2.63	-17.23	
15	208657_s_at	MSF	-6.86	1.07E-19	4.13E-17	-2.32	-16.86	17q25
16	206111_at	RNASE2	31.57	9.90E-18	1.55E-15	2.60	16.77	14q24-q31
17	209374_s_at	IGHM	-20.50	2.26E-19	7.67E-17	-2.31	-16.64	14q32.33
18	213737_x_at		4.04	1.90E-18	4.34E-16	2.37	16.63	
19	209075_s_at	NIFU	-3.01	2.08E-23	4.94E-20	-2.05	-16.58	12q24.1
20	212590_at	RRAS2	-11.91	8.40E-19	2.27E-16	-2.38	-16.56	11p15.2
21	39582_at		-4.91	4.97E-20	2.23E-17	-2.19	-16.44	
22	215785_s_at	CYFIP2	-9.58	2.53E-20	1.31E-17	-2.16	-16.42	5q34
23	208944_at	TGFBR2	-4.11	1.74E-22	2.01E-19	-2.02	-16.25	3p22
24	41577_at	PPP1R16B	-9.45	7.42E-21	5.14E-18	-2.09	-16.22	20q11.23
25	212589_at	RRAS2	-25.69	4.92E-18	8.79E-16	-2.42	-16.09	11p15.2
26	212750_at	PPP1R16B	-7.28	8.90E-23	1.23E-19	-1.98	-16.06	20q11.23
27	212313_at	MGC29816	-6.02	1.93E-18	4.34E-16	-2.24	-15.87	8p21.2
28	208456_s_at	RRAS2	-16.84	7.02E-18	1.19E-15	-2.35	-15.83	11p15.2
29	214615_at	P2RY10	-11.66	4.87E-18	8.79E-16	-2.28	-15.75	Xq21.1
30	201648_at		-2.80	1.31E-21	9.91E-19	-1.95	-15.62	
31	229844_at		-6.66	7.08E-18	1.19E-15	-2.25	-15.56	
32	223391_at	SGPP1	-17.31	2.66E-18	5.52E-16	-2.17	-15.54	14q23.1
33	226508_at		-4.47	1.20E-18	2.98E-16	-2.11	-15.49	
34	214651_s_at	HOXA9	199.29	2.35E-16	2.10E-14	2.66	15.40	7p15-p14
35	224482_s_at	RAB11-FIP4	-7.81	2.08E-20	1.24E-17	-1.96	-15.39	
36	211404_s_at	APLP2	5.26	2.79E-18	5.72E-16	2.07	15.33	11q24
37	AFFX-HUMGAPDH/M33197_3_at - HG-U133B	GAPD	2.28	1.21E-22	1.54E-19	1.87	15.33	12p13
38	228390_at		-46.90	2.89E-17	3.78E-15	-2.35	-15.33	
39	208091_s_at	DKFZP564K0822	-7.35	3.43E-18	6.62E-16	-2.12	-15.31	7p14.1
40	223287_s_at	FOXP1	-4.95	1.93E-18	4.34E-16	-2.08	-15.27	3p14.1
41	207000_s_at	PPP3CC	-5.93	7.39E-19	2.08E-16	-2.04	-15.27	8p21.2
42	202863_at	SP100	-3.35	4.98E-19	1.48E-16	-2.02	-15.26	2q37.1
43	224709_s_at	SPEC2	-2.68	2.88E-23	5.99E-20	-1.84	-15.25	5q31.1
44	234734_s_at	TNRC6	-2.60	1.06E-21	8.34E-19	-1.88	-15.25	16p11.2
45	213295_at		-4.06	1.42E-19	5.23E-17	-1.98	-15.23	
46	227670_at	ZNF75A	-5.65	4.99E-19	1.48E-16	-2.00	-15.18	16p13.11
47	226331_at		-3.59	3.76E-23	6.94E-20	-1.83	-15.16	
48	233849_s_at	ARHGAP5	-12.51	3.55E-19	1.13E-16	-1.98	-15.14	14q12
49	AFFX-HUMGAPDH/M33197_3_at - HG-U133A	GAPD	2.19	1.81E-22	2.01E-19	1.84	15.11	12p13
50	212386_at		-17.35	6.03E-18	1.05E-15	-2.09	-15.09	
2.49	AML_MLL versus CML							

Table 2.1-2.78

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	206676_at	CEACAM8	-27.77	7.07E-33	2.11E-29	-3.29	-26.88	19q13.2
2	212531_at	LCN2	-22.72	2.13E-34	9.55E-31	-3.09	-26.28	9q34
3	209771_x_at	CD24	-13.42	1.81E-36	1.62E-32	-2.94	-25.80	6q21
4	216379_x_at	KIAA1919	-15.24	1.45E-34	8.63E-31	-2.96	-25.51	6q22
5	205557_at	BPI	-10.70	1.66E-37	2.97E-33	-2.69	-24.22	20q11.23-q12
6	211657_at	CEACAM6	-17.83	1.18E-32	3.02E-29	-2.68	-23.20	19q13.2
7	203757_s_at	CEACAM6	-28.13	9.61E-30	1.91E-26	-2.80	-23.02	19q13.2
8	208650_s_at	CD24	-29.40	6.44E-27	8.63E-24	-2.71	-21.27	6q21
9	205513_at	TCN1	-19.93	1.70E-27	2.76E-24	-2.62	-21.19	11q11-q12
10	203021_at	SLPI	-9.07	5.59E-28	1.00E-24	-2.57	-21.15	20q12
11	201061_s_at	STOM	-5.35	3.04E-31	6.79E-28	-2.40	-21.10	9q34.1
12	202018_s_at	LTF	-9.14	6.96E-34	2.49E-30	-2.31	-20.89	3q21-q23
13	266_s_at	CD24	-20.66	9.11E-27	1.09E-23	-2.56	-20.61	6q21
14	210244_at	CAMP	-31.74	1.46E-25	1.13E-22	-2.57	-20.00	3p21.3
15	209772_s_at	CD24	-42.41	4.50E-25	3.22E-22	-2.61	-19.80	6q21
16	207802_at	SGP28	-54.67	4.75E-25	3.27E-22	-2.51	-19.51	6p12.3
17	209396_s_at	CHI3L1	-31.25	3.93E-24	2.20E-21	-2.44	-18.74	1q32.1
18	208651_x_at	CD24	-11.30	3.48E-26	3.67E-23	-2.09	-18.01	6q21
19	203936_s_at	MMP9	-13.29	1.23E-25	1.00E-22	-2.08	-17.79	20q11.2-q13.1
20	201060_x_at	STOM	-5.38	6.78E-26	6.07E-23	-2.03	-17.58	9q34.1
21	209369_at	ANXA3	-18.37	4.42E-24	2.27E-21	-2.13	-17.55	4q13-q22
22	224967_at	UGCG	-6.19	1.42E-26	1.59E-23	-1.97	-17.32	9q31
23	230006_s_at	DKFZp313A2432	-6.65	4.44E-24	2.27E-21	-1.99	-16.83	11p14.2
24	201554_x_at	GYG	-3.92	3.30E-27	4.92E-24	-1.81	-16.38	3q24-q25.1
25	226278_at	DKFZp313A2432	-5.99	3.11E-24	1.79E-21	-1.90	-16.37	11p14.2
26	210140_at	CST7	-5.33	6.75E-27	8.63E-24	-1.79	-16.19	20p11.21
27	231688_at		-8.54	4.12E-26	3.88E-23	-1.79	-16.09	
28	219281_at	MSRA	-3.01	1.06E-24	6.54E-22	-1.83	-16.07	8p23.1
29	207269_at	DEFA4	-7.80	8.84E-26	7.53E-23	-1.77	-15.94	8p23
30	230285_at	DKFZp313A2432	-6.50	2.57E-22	1.05E-19	-1.90	-15.84	11p14.2
31	236979_at		-4.55	5.45E-22	2.07E-19	-1.92	-15.81	
32	206871_at	ELA2	-4.21	1.20E-23	5.94E-21	-1.79	-15.73	19p13.3
33	211275_s_at	GYG	-3.02	3.90E-26	3.88E-23	-1.74	-15.71	3q24-q25.1
34	201905_s_at	HYA22	-6.24	1.34E-24	8.00E-22	-1.77	-15.67	3p21.3
35	206207_at	CLC	-9.87	5.37E-25	3.56E-22	-1.72	-15.44	19q13.1
36	200985_s_at	CD59	-7.59	2.00E-23	9.41E-21	-1.75	-15.33	11p13
37	214953_s_at	APP	-8.96	1.23E-23	5.94E-21	-1.73	-15.27	21q21.3
38	202252_at	RAB13	-3.03	3.48E-25	2.59E-22	-1.68	-15.22	1q21.2
39	234317_s_at	DKFZp762K222	-5.51	2.70E-21	9.30E-19	-1.84	-15.20	4q35.1
40	206656_s_at	C20orf3	-3.26	4.13E-24	2.24E-21	-1.70	-15.16	20p11.22-p11.21
41	209447_at	SYNE1	-8.48	6.26E-21	1.96E-18	-1.86	-15.13	6q25
42	223423_at	GPCR1	-3.50	8.78E-25	5.61E-22	-1.68	-15.12	3q26.2-q27
43	225829_at	LOC118987	-6.43	1.25E-21	4.39E-19	-1.79	-15.06	10q26.12
44	204881_s_at	UGCG	-8.18	4.33E-21	1.41E-18	-1.80	-14.95	9q31
45	209395_at	CHI3L1	-72.69	1.00E-19	2.72E-17	-2.03	-14.91	1q32.1

Table 2.1-2.78

46	224707_at	ORF1-FL49	-5.25	3.25E-21	1.10E-18	-1.78	-14.89	5q31.3
47	201904_s_at	HYA22	-10.51	2.35E-22	9.78E-20	-1.70	-14.79	3p21.3
48	202119_s_at	CPNE3	-6.86	8.93E-22	3.33E-19	-1.72	-14.78	8q21.13
49	204411_at	KIAA0449	-8.27	7.46E-23	3.18E-20	-1.66	-14.70	1pter-q31.3
50	217762_s_at	RAB31	-5.79	2.92E-23	1.31E-20	-1.65	-14.67	18p11.3
2.50	AML_MLL versus normalBM							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	202018_s_at	LTF	-9.66	2.68E-10	1.20E-07	-3.31	-17.59	3q21-q23
2	214651_s_at	HOXA9	30.37	4.97E-16	6.89E-12	2.54	14.95	7p15-p14
3	235733_at		-3.04	3.20E-11	2.46E-08	-2.38	-13.93	
4	228716_at		-4.24	2.87E-09	7.95E-07	-2.49	-13.53	
5	227041_at		-2.61	8.52E-12	9.84E-09	-2.14	-12.98	
6	212531_at	LCN2	-20.69	6.47E-07	3.79E-05	-3.25	-12.96	9q34
7	214109_at	LRBA	-1.95	6.29E-15	4.35E-11	-1.93	-12.44	4q31.22-q31.23
8	213737_x_at		2.56	3.00E-14	1.38E-10	1.82	11.73	
9	225792_at		-4.45	7.07E-07	3.89E-05	-2.43	-11.20	
10	201105_at	LGALS1	5.54	9.84E-14	3.41E-10	1.71	11.06	22q13.1
11	209905_at	HOXA9	156.33	2.07E-12	3.19E-09	1.90	11.00	7p15-p14
12	213147_at	HOXA10	6.85	2.03E-13	5.48E-10	1.71	11.00	7p15-p14
13	235753_at		6.91	9.30E-13	1.84E-09	1.76	10.95	
14	206847_s_at	HOXA7	7.31	2.37E-13	5.48E-10	1.67	10.79	7p15-p14
15	225923_at		-2.10	6.23E-10	2.40E-07	-1.78	-10.69	
16	205849_s_at	UQCRB	1.98	6.58E-10	2.46E-07	1.74	10.50	8q22
17	217979_at	NET-6	-3.89	2.16E-08	3.48E-06	-1.85	-10.42	7p21.1
18	210192_at	ATP8A1	-2.79	5.95E-08	6.99E-06	-1.86	-10.26	4p14-p12
19	202265_at	BMI1	5.04	3.15E-12	4.36E-09	1.62	10.25	10p11.23
20	208651_x_at	CD24	-8.71	2.18E-06	8.71E-05	-2.30	-10.25	6q21
21	229860_x_at		3.92	1.24E-12	2.15E-09	1.57	10.18	
22	228083_at	CACNA2D4	12.06	1.69E-11	1.46E-08	1.64	9.99	12p13.33
23	217047_s_at	FAM13A1	-2.90	2.62E-10	1.20E-07	-1.60	-9.91	4q22.1
24	237444_at		-2.68	7.69E-09	1.64E-06	-1.68	-9.89	
25	224767_at		5.87	8.27E-12	9.84E-09	1.55	9.84	
26	209771_x_at	CD24	-10.88	5.64E-06	1.65E-04	-2.38	-9.75	6q21
27	200631_s_at	SET	1.63	1.08E-11	1.15E-08	1.48	9.57	9q34
28	216379_x_at	KIAA1919	-12.73	8.00E-06	2.08E-04	-2.44	-9.56	6q22
29	205624_at	CPA3	-4.24	1.04E-07	1.06E-05	-1.70	-9.49	3q21-q25
30	221030_s_at	DKFZP564B1162	-2.62	7.20E-08	8.24E-06	-1.67	-9.46	4q21.3
31	202561_at	TNKS	-2.22	6.05E-10	2.40E-07	-1.51	-9.40	8p23.1
32	201268_at	NME2	2.34	1.47E-10	8.17E-08	1.48	9.38	17q21.3
33	209066_x_at	UQCRB	2.48	1.23E-11	1.21E-08	1.45	9.37	8q22
34	201162_at	IGFBP7	5.03	3.56E-11	2.59E-08	1.48	9.37	4q12
35	201135_at	ECHS1	2.33	1.65E-11	1.46E-08	1.44	9.29	10q26.2-q26.3
36	227812_at		-3.41	4.97E-06	1.53E-04	-2.06	-9.26	

37	214785_at	CHAC	-2.05	5.14E-08	6.36E-06	-1.61	-9.25	9q21
38	205033_s_at	DEFA1	-4.06	1.08E-07	1.08E-05	-1.64	-9.24	8p23.2-p23.1
39	225464_at	C14orf31	-2.82	3.87E-09	9.59E-07	-1.51	-9.21	14q21.3
40	209329_x_at	MGC2198	1.93	2.29E-11	1.86E-08	1.42	9.18	5q35.3
41	225700_at	GLCCI1	-3.81	8.54E-06	2.14E-04	-2.16	-9.11	7p22.1
42	211404_s_at	APLP2	2.19	5.47E-11	3.61E-08	1.41	9.08	11q24
43	226301_at	dJ55C23.6	-4.12	4.34E-09	1.06E-06	-1.49	-9.06	6q22.3-q23.3
44	213150_at	HOXA10	8.08	1.86E-10	9.53E-08	1.49	9.05	7p15-p14
45	209036_s_at	MDH2	1.92	8.33E-11	5.25E-08	1.41	9.04	7p12.3-q11.2
46	40189_at	SET	1.69	4.19E-11	2.90E-08	1.40	9.03	9q34
47	211662_s_at	VDAC2	1.83	1.58E-10	8.43E-08	1.41	9.01	10q22
48	227448_at		-2.18	1.26E-07	1.22E-05	-1.58	-8.98	
49	203734_at	FHX	-1.79	9.97E-08	1.03E-05	-1.56	-8.93	12p13.31
50	227545_at		-2.13	2.15E-06	8.63E-05	-1.77	-8.88	
2.51	AML_inv(16) versus AML_inv(3)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	203949_at	MPO	4.50	1.34E-17	3.70E-13	2.52	16.16	17q23.1
2	203948_s_at	MPO	5.13	3.61E-16	4.97E-12	2.05	13.37	17q23.1
3	205382_s_at	DF	5.63	3.26E-13	2.99E-09	1.85	11.66	19p13.3
4	201497_x_at	MYH11	19.05	6.47E-11	3.56E-07	2.09	11.02	16p13.13-p13.12
5	209365_s_at	ECM1	3.55	3.80E-12	2.62E-08	1.68	10.58	1q21
6	210755_at	HGF	6.55	1.77E-10	6.09E-07	1.70	9.96	7q21.1
7	217963_s_at	NGFRAP1	-22.83	1.95E-08	1.45E-05	-1.97	-9.62	Xq22.1
8	205718_at	ITGB7	3.13	8.99E-11	4.12E-07	1.41	9.03	12q13.13
9	208248_x_at	APLP2	2.15	1.31E-10	5.17E-07	1.35	8.78	11q24
10	202605_at	GUSB	2.31	2.30E-10	7.03E-07	1.35	8.72	7q21.11
11	224841_x_at		-1.65	4.68E-09	5.86E-06	-1.42	-8.60	
12	224741_x_at		-1.65	4.37E-09	5.73E-06	-1.41	-8.57	
13	200985_s_at	CD59	-7.88	6.95E-08	3.10E-05	-1.58	-8.43	11p13
14	223136_at	AIG-1	-5.64	1.52E-08	1.25E-05	-1.40	-8.33	6q24.1
15	222862_s_at	AK5	27.90	1.73E-08	1.36E-05	1.54	8.23	1p31
16	201496_x_at	MYH11	3.43	1.98E-09	4.53E-06	1.31	8.22	16p13.13-p13.12
17	211709_s_at	SCGF	3.66	3.59E-10	9.87E-07	1.25	8.20	19q13.3
18	212358_at	CLIPR-59	18.74	2.53E-08	1.66E-05	1.56	8.09	19q13.12
19	226197_at		2.63	3.14E-09	4.93E-06	1.25	7.94	
20	200984_s_at	CD59	-3.23	8.03E-08	3.39E-05	-1.39	-7.92	11p13
21	218217_at	RISC	2.67	3.47E-09	4.93E-06	1.24	7.88	17q23.1
22	201462_at	KIAA0193	-5.53	4.85E-08	2.30E-05	-1.33	-7.86	7p14.3-p14.1
23	210997_at	HGF	22.58	4.15E-08	2.12E-05	1.46	7.82	7q21.1
24	226121_at	MGC23280	-2.43	3.57E-08	1.91E-05	-1.30	-7.81	17q11.1
25	228497_at	FLIPT1	-3.42	1.25E-07	4.52E-05	-1.39	-7.80	1p13.1
26	208702_x_at	APLP2	2.40	2.97E-09	4.93E-06	1.20	7.78	11q24
27	220668_s_at	DNMT3B	-5.06	3.67E-07	9.36E-05	-1.54	-7.76	20q11.2

Table 2.1-2.78

28	214875_x_at	APLP2	2.55	1.88E-09	4.53E-06	1.19	7.75	11q24
29	207961_x_at	MYH11	13.58	5.40E-08	2.52E-05	1.43	7.71	16p13.13-p13.12
30	204198_s_at	RUNX3	-5.88	2.49E-07	7.54E-05	-1.42	-7.69	1p36
31	201029_s_at	CD99	1.55	1.51E-08	1.25E-05	1.23	7.67	Xp22.32
32	205076_s_at	CRA	4.58	4.39E-08	2.16E-05	1.35	7.66	1q12-q21
33	231736_x_at	MGST1	3.21	2.85E-09	4.93E-06	1.16	7.56	12p12.3-p12.1
34	223640_at	PIK3AP	2.38	3.34E-09	4.93E-06	1.15	7.53	19q13.1
35	200078_s_at - HG-U133B	ATP6V0B	2.01	3.17E-09	4.93E-06	1.15	7.51	1p32.3
36	209975_at	CYP2E1	3.78	2.34E-08	1.61E-05	1.22	7.50	10q24.3-qter
37	224918_x_at	MGST1	2.97	3.48E-09	4.93E-06	1.14	7.49	12p12.3-p12.1
38	202185_at	PLOD3	1.83	3.58E-09	4.93E-06	1.14	7.49	7q22
39	200872_at	S100A10	3.00	7.76E-09	7.90E-06	1.16	7.47	1q21
40	241525_at	LOC200772	37.93	9.78E-08	3.74E-05	1.41	7.47	2q37.3
41	230896_at		-41.32	9.11E-07	1.71E-04	-1.70	-7.47	
42	208704_x_at	APLP2	2.39	4.96E-09	5.93E-06	1.14	7.44	11q24
43	243244_at		3.09	6.78E-09	7.47E-06	1.14	7.41	
44	212463_at		-4.59	5.24E-07	1.13E-04	-1.39	-7.39	
45	202283_at	SERPINF1	4.66	2.32E-08	1.61E-05	1.17	7.33	17p13.1
46	205859_at	LY86	3.57	7.41E-09	7.84E-06	1.12	7.32	6p24.3
47	204122_at	TYROBP	2.73	6.45E-09	7.40E-06	1.12	7.31	19q13.1
48	223091_x_at	GL004	-1.53	1.84E-08	1.41E-05	-1.14	-7.30	2q36.3
49	205131_x_at	SCGF	4.95	3.38E-08	1.90E-05	1.17	7.29	19q13.3
50	238151_at		2.68	3.62E-08	1.91E-05	1.16	7.27	
2.52	AML_inv(16) versus AML_komplext							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	209190_s_at	DIAPH1	2.58	2.08E-14	1.34E-10	1.64	11.80	5q31
2	201497_x_at	MYH11	20.34	5.66E-11	2.80E-08	2.00	11.03	16p13.13-p13.12
3	201496_x_at	MYH11	8.16	1.93E-11	1.38E-08	1.63	10.61	16p13.13-p13.12
4	200984_s_at	CD59	-5.61	1.78E-12	3.27E-09	-1.54	-10.44	11p13
5	212463_at		-8.87	3.40E-12	4.96E-09	-1.59	-10.41	
6	209619_at	CD74	2.48	3.74E-13	9.64E-10	1.42	10.41	5q32
7	222229_x_at		1.45	1.28E-14	1.34E-10	1.35	10.37	
8	200985_s_at	CD59	-13.21	5.81E-12	6.02E-09	-1.54	-10.16	11p13
9	200093_s_at - HG-U133B	HINT1	1.79	8.03E-14	3.45E-10	1.28	9.82	5q31.2
10	205382_s_at	DF	3.68	3.91E-12	5.04E-09	1.31	9.62	19p13.3
11	206847_s_at	HOXA7	-3.70	1.36E-12	2.91E-09	-1.30	-9.60	7p15-p14
12	217846_at	QARS	1.68	3.05E-13	9.64E-10	1.24	9.52	3p21.3-p21.1
13	232247_at	FLJ14855	-2.34	1.13E-11	9.74E-09	-1.26	-9.18	3p21.31
14	204198_s_at	RUNX3	-7.48	5.36E-11	2.76E-08	-1.33	-9.13	1p36
15	208886_at	H1F0	-5.94	4.78E-11	2.56E-08	-1.28	-9.01	22q13.1
16	207332_s_at	TFRC	-2.71	6.34E-11	2.90E-08	-1.29	-8.98	3q26.2-qter

Table 2.1-2.78

17	201360_at	CST3	4.32	4.84E-10	1.18E-07	1.34	8.97	20p11.21
18	241706_at	LOC144402	-5.96	4.36E-11	2.56E-08	-1.26	-8.96	12q11
19	202413_s_at	USP1	-1.86	3.47E-12	4.96E-09	-1.16	-8.85	1p32.1-p31.3
20	223276_at	NID67	2.53	9.44E-11	3.80E-08	1.23	8.85	5q33.1
21	217963_s_at	NGFRAP1	-19.01	2.22E-10	6.97E-08	-1.35	-8.83	Xq22.1
22	200675_at	CD81	-3.56	6.30E-12	6.02E-09	-1.16	-8.82	11p15.5
23	218040_at	FLJ10330	-2.22	6.54E-12	6.02E-09	-1.16	-8.82	1p13.2
24	210715_s_at	SPINT2	-3.66	1.37E-11	1.10E-08	-1.17	-8.76	19q13.1
25	209523_at	TAF2	-2.75	5.20E-12	6.02E-09	-1.14	-8.74	8q24.12
26	244552_at		-4.00	6.01E-11	2.86E-08	-1.19	-8.64	
27	200983_x_at	CD59	-8.23	3.32E-10	9.44E-08	-1.29	-8.61	11p13
28	244741_s_at		-6.23	3.17E-10	9.29E-08	-1.27	-8.58	
29	235753_at		-6.27	5.94E-10	1.32E-07	-1.32	-8.50	
30	200665_s_at	SPARC	3.15	4.51E-11	2.56E-08	1.13	8.49	5q31.3-q32
31	202406_s_at	TIAL1	-1.66	1.81E-11	1.37E-08	-1.11	-8.47	10q
32	213779_at	LOC129080	-3.29	1.78E-10	5.89E-08	-1.19	-8.46	22q12.1
33	212066_s_at	KIAA0570	-1.86	4.63E-11	2.56E-08	-1.12	-8.39	2p14
34	208033_s_at	ATBF1	3.73	1.09E-09	1.97E-07	1.20	8.35	16q22.3-q23.1
35	224724_at	SULF2	5.32	3.98E-09	4.79E-07	1.29	8.35	20q12-13.2
36	214651_s_at	HOXA9	-11.93	7.94E-10	1.57E-07	-1.26	-8.34	7p15-p14
37	225383_at	ZNF275	-1.92	8.65E-11	3.59E-08	-1.12	-8.32	Xq28
38	213737_x_at		-2.31	1.73E-10	5.89E-08	-1.14	-8.30	
39	201663_s_at	SMC4L1	-2.67	2.46E-10	7.54E-08	-1.14	-8.26	3q26.1
40	203965_at	USP20	-2.20	3.14E-11	2.13E-08	-1.07	-8.21	9q34.13
41	205718_at	ITGB7	3.46	6.54E-11	2.90E-08	1.08	8.20	12q13.13
42	218414_s_at	NUDE1	-2.89	7.27E-10	1.49E-07	-1.19	-8.19	16p13.11
43	201377_at	NICE-4	-1.89	8.01E-11	3.44E-08	-1.08	-8.16	1q21.3
44	212826_s_at	SLC25A6	1.63	3.95E-11	2.54E-08	1.06	8.15	Xp22.32 and Yp
45	223769_x_at	HT036	-2.28	3.80E-10	1.01E-07	-1.13	-8.13	1p34.1
46	202265_at	BMI1	-2.97	4.98E-10	1.18E-07	-1.13	-8.10	10p11.23
47	230219_at	NUDE1	-2.08	1.63E-10	5.82E-08	-1.08	-8.10	16p13.11
48	207992_s_at	AMPD3	-2.91	3.85E-10	1.01E-07	-1.11	-8.08	11p15
49	200620_at	C1orf8	-1.54	1.23E-10	4.67E-08	-1.07	-8.05	1p36-p31
50	208691_at	TFRC	-2.54	8.50E-10	1.63E-07	-1.14	-8.04	3q26.2-qter
2.53	AML_inv(16) versus AML_t(15;17)							
#	affy Id	HUGO name	fc	p	q	stn	t	Map Location
1	211990_at	HLA-DPA1	12.87	6.59E-19	1.76E-14	3.40	20.83	6p21.3
2	214450_at	CTSW	-7.68	6.17E-13	5.50E-10	-2.95	-15.78	11q13.1
3	204661_at	CDW52	33.90	2.84E-14	7.34E-11	2.75	15.39	1p36
4	38487_at	STAB1	-7.92	2.48E-12	1.89E-09	-3.00	-15.22	3p21.31
5	209732_at	CLECSF2	30.41	1.19E-13	1.77E-10	2.75	14.76	12p13-p12
6	217478_s_at	HLA-DMA	7.72	5.11E-15	2.13E-11	2.38	14.68	6p21.3
7	221004_s_at	ITM2C	-4.93	9.59E-14	1.51E-10	-2.43	-14.58	2q37

Table 2.1-2.78

8	34210_at	CDW52	43.95	1.36E-13	1.92E-10	2.64	14.51	1p36
9	200654_at	P4HB	-2.26	2.17E-15	1.16E-11	-2.24	-14.34	17q25
10	203535_at	S100A9	8.87	5.77E-16	5.14E-12	2.17	14.08	1q21
11	209619_at	CD74	5.65	4.69E-17	6.26E-13	2.09	13.92	5q32
12	238022_at		-8.04	2.75E-12	2.00E-09	-2.31	-13.37	
13	200931_s_at	VCL	3.99	1.89E-15	1.16E-11	2.04	13.29	10q22.1-q23
14	201923_at	PRDX4	7.40	5.83E-14	1.11E-10	2.12	13.18	Xp22.13
15	209312_x_at	HLA-DRB1	8.91	4.83E-14	9.92E-11	2.10	13.11	6p21.3
16	208306_x_at	HLA-DRB4	9.68	8.26E-14	1.47E-10	2.12	13.11	6p21.3
17	205624_at	CPA3	-8.88	1.01E-11	5.61E-09	-2.34	-13.07	3q21-q25
18	204563_at	SELL	9.19	5.06E-13	5.01E-10	2.18	12.90	1q23-q25
19	204670_x_at	HLA-DRB5	6.82	5.58E-15	2.13E-11	1.94	12.69	6p21.3
20	231310_at		4.86	4.39E-14	9.77E-11	1.98	12.63	
21	208891_at	DUSP6	7.87	1.16E-14	3.88E-11	1.92	12.52	12q22-q23
22	212953_x_at	CALR	-2.83	3.00E-14	7.34E-11	-1.93	-12.49	19p13.3-p13.2
23	238365_s_at		-10.18	1.04E-10	3.05E-08	-2.44	-12.36	
24	207375_s_at	IL15RA	4.86	3.02E-14	7.34E-11	1.86	12.14	10p15-p14
25	221059_s_at	CHST6	6.79	8.00E-13	6.89E-10	1.98	12.11	16q22
26	208982_at	PECAM1	4.84	3.84E-13	4.22E-10	1.91	11.99	17q23
27	205718_at	ITGB7	6.51	4.60E-13	4.72E-10	1.91	11.97	12q13.13
28	205663_at	PCBP3	-4.82	1.21E-11	6.17E-09	-2.01	-11.95	21q22.3
29	229168_at	DKFZp434K0621	-6.66	3.87E-10	8.47E-08	-2.35	-11.57	5q35.3
30	233072_at	KIAA1857	-7.11	2.16E-10	5.54E-08	-2.13	-11.47	9q34
31	211991_s_at	HLA-DPA1	25.47	2.35E-11	1.07E-08	2.09	11.45	6p21.3
32	224583_at	COTL1	5.47	3.94E-13	4.22E-10	1.78	11.44	16q23.3
33	232617_at	CTSS	8.68	2.07E-11	9.71E-09	2.05	11.43	1q21
34	224839_s_at	GPT2	-8.67	4.98E-11	1.73E-08	-1.95	-11.38	16q12.1
35	201497_x_at	MYH11	29.05	4.61E-11	1.65E-08	2.19	11.25	16p13.13-p13.12
36	241742_at	PRAM-1	11.62	2.96E-11	1.22E-08	2.01	11.23	19p13.2
37	226878_at		4.23	4.00E-12	2.61E-09	1.81	11.18	
38	201137_s_at	HLA-DPB1	15.27	5.30E-11	1.81E-08	1.99	10.99	6p21.3
39	208689_s_at	RPN2	-1.74	1.74E-13	2.32E-10	-1.65	-10.96	20q12-q13.1
40	201496_x_at	MYH11	10.95	8.48E-12	5.03E-09	1.78	10.95	16p13.13-p13.12
41	202803_s_at	ITGB2	5.33	5.45E-13	5.20E-10	1.66	10.86	21q22.3
42	204150_at	STAB1	-9.25	1.13E-09	2.11E-07	-2.20	-10.85	3p21.31
43	238376_at		3.13	1.34E-12	1.11E-09	1.68	10.82	
44	202820_at	AHR	7.11	2.91E-12	2.05E-09	1.69	10.77	7p15
45	202644_s_at	TNFAIP3	2.63	9.42E-14	1.51E-10	1.60	10.76	6q23
46	223280_x_at	MS4A6A	24.32	1.17E-10	3.37E-08	2.00	10.68	11q12.1
47	228046_at	LOC152485	3.11	5.33E-12	3.39E-09	1.69	10.68	4q31.1
48	228113_at	STAT3	3.41	2.65E-13	3.31E-10	1.60	10.63	17q21
49	213779_at	LOC129080	-6.48	1.04E-09	1.96E-07	-2.02	-10.63	22q12.1
50	210982_s_at	HLA-DRA	7.45	1.37E-12	1.11E-09	1.63	10.60	6p21.3
2.54	AML_inv(16) versus AML_t(8;21)							

Table 2.1-2.78

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	207075_at	CIAS1	6.20	6.53E-13	4.40E-09	2.14	12.84	1q44
2	205718_at	ITGB7	7.97	2.06E-13	2.37E-09	1.94	12.42	12q13.13
3	208890_s_at	PLXNB2	5.47	2.82E-13	2.37E-09	1.95	12.41	22q13.33
4	224764_at	ARHGAP10	9.78	6.18E-12	1.89E-08	2.04	11.88	10
5	205419_at	EBI2	7.28	3.55E-12	1.52E-08	1.93	11.76	13q32.2
6	218795_at	ACP6	-4.43	2.56E-13	2.37E-09	-1.71	-11.41	1q21
7	224049_at	KCNK17	4.96	2.15E-11	5.57E-08	1.93	11.23	6p21.1
8	201497_x_at	MYH11	27.72	4.77E-11	7.64E-08	2.18	11.23	16p13.13-p13.12
9	218236_s_at	PRKCN	5.61	2.01E-12	1.13E-08	1.65	10.88	2p21
10	238604_at		3.46	2.13E-13	2.37E-09	1.50	10.47	
11	205453_at	HOXB2	15.78	1.65E-10	1.74E-07	1.88	10.41	17q21-q22
12	201596_x_at	KRT18	9.11	3.90E-11	6.91E-08	1.67	10.37	12q13
13	224724_at	SULF2	26.58	2.51E-10	2.26E-07	1.96	10.31	20q12-13.2
14	209365_s_at	ECM1	3.32	5.67E-12	1.89E-08	1.52	10.17	1q21
15	228827_at		-100.56	4.49E-10	3.22E-07	-1.97	-10.04	
16	201496_x_at	MYH11	6.61	2.98E-11	6.14E-08	1.55	10.02	16p13.13-p13.12
17	200665_s_at	SPARC	3.67	6.00E-12	1.89E-08	1.49	10.02	5q31.3-q32
18	201739_at	SGK	4.55	3.60E-12	1.52E-08	1.46	9.97	6q23
19	201944_at	HEXB	2.26	3.09E-11	6.14E-08	1.52	9.92	5q13
20	209500_x_at	TNFSF13	4.26	1.51E-10	1.70E-07	1.52	9.61	17p13.1
21	235359_at		3.06	5.86E-11	8.57E-08	1.46	9.56	
22	203320_at	LNK	2.89	7.98E-11	1.12E-07	1.47	9.56	12q24
23	208683_at	CAPN2	3.25	1.30E-11	3.66E-08	1.39	9.47	1q41-q42
24	211084_x_at	PRKCN	4.90	2.81E-11	6.14E-08	1.40	9.46	2p21
25	217849_s_at	CDC42BPB	5.22	3.31E-11	6.19E-08	1.41	9.46	14q32.3
26	210314_x_at	TNFSF13	5.02	1.80E-10	1.80E-07	1.48	9.45	17p13.1
27	206940_s_at	POU4F1	-37.07	1.50E-09	8.29E-07	-1.82	-9.42	13q21.1-q22
28	201887_at	IL13RA1	4.32	3.65E-10	2.73E-07	1.52	9.40	Xq24
29	223249_at	CLDN12	3.44	5.41E-11	8.27E-08	1.41	9.40	7q21
30	240572_s_at		3.50	3.10E-11	6.14E-08	1.39	9.40	
31	220974_x_at	BA108L7.2	4.98	1.02E-10	1.33E-07	1.39	9.22	10q24.31
32	205529_s_at	CBFA2T1	-14.03	2.39E-09	1.17E-06	-1.70	-9.16	8q22
33	236738_at		7.02	4.91E-10	3.38E-07	1.44	9.10	
34	201005_at	CD9	7.50	3.32E-10	2.65E-07	1.40	9.04	12p13.3
35	201360_at	CST3	4.55	3.35E-10	2.65E-07	1.39	9.02	20p11.21
36	225102_at	LOC152009	-3.87	3.38E-10	2.65E-07	-1.34	-8.83	3q21.3
37	218237_s_at	SLC38A1	3.46	4.08E-10	2.98E-07	1.35	8.82	12q12
38	205330_at	MN1	9.47	3.99E-09	1.74E-06	1.56	8.81	22q12.1
39	225602_at	C9orf19	2.74	4.53E-11	7.63E-08	1.26	8.75	9p13-p12
40	220591_s_at	FLJ22843	3.10	7.60E-10	4.74E-07	1.35	8.72	Xp11.3
41	229309_at		10.85	4.42E-09	1.91E-06	1.52	8.71	
42	229383_at		5.16	3.78E-09	1.67E-06	1.46	8.66	
43	201425_at	ALDH2	6.54	3.46E-10	2.65E-07	1.29	8.64	12q24.2

Table 2.1-2.78

44	229406_at		-8.50	3.12E-09	1.48E-06	-1.43	-8.63	
45	208033_s_at	ATBF1	4.00	6.81E-10	4.41E-07	1.30	8.57	16q22.3-q23.1
46	205859_at	LY86	3.64	2.66E-09	1.28E-06	1.38	8.57	6p24.3
47	211341_at	POU4F1	-162.01	1.01E-08	3.29E-06	-1.68	-8.52	13q21.1-q22
48	224579_at		3.69	1.71E-09	9.28E-07	1.33	8.52	
49	202283_at	SERPINF1	8.19	2.29E-09	1.15E-06	1.35	8.51	17p13.1
50	226818_at	LOC219972	10.78	6.29E-09	2.38E-06	1.45	8.48	11q12.1
2.55	AML_inv(16) versus CLL							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	203949_at	MPO	140.69	6.50E-22	8.85E-19	6.40	34.02	17q23.1
2	224838_at	FOXP1	-5.75	4.76E-28	8.42E-24	-3.73	-26.98	3p14.1
3	203948_s_at	MPO	228.28	2.74E-18	9.63E-16	4.62	23.95	17q23.1
4	207168_s_at	H2AFY	3.02	4.10E-27	3.63E-23	2.81	21.50	5q31.3-q32
5	212827_at	IGHM	-22.96	2.32E-21	2.74E-18	-3.15	-20.49	14q32.33
6	223514_at	CARD11	-42.77	5.00E-20	3.54E-17	-3.10	-18.99	7p22
7	201029_s_at	CD99	2.32	1.78E-23	4.49E-20	2.37	18.11	Xp22.32
8	AFFX-HUMGAPDH/M33197_3_at - HG-U133B	GAPD	2.23	1.84E-25	1.08E-21	2.30	17.95	12p13
9	201811_x_at	SH3BP5	-11.14	9.30E-21	9.14E-18	-2.48	-17.75	3p24.3
10	224837_at	FOXP1	-3.53	1.38E-21	1.74E-18	-2.39	-17.61	3p14.1
11	41220_at	MSF	-2.10	4.06E-25	1.80E-21	-2.25	-17.57	17q25
12	201012_at	ANXA1	5.40	2.01E-22	3.24E-19	2.29	17.38	9q12-q21.2
13	243780_at		-36.28	8.86E-19	3.91E-16	-2.76	-17.28	
14	200650_s_at	LDHA	2.62	2.64E-24	9.35E-21	2.18	17.03	11p15.4
15	209374_s_at	IGHM	-19.86	9.06E-19	3.91E-16	-2.60	-16.99	14q32.33
16	209075_s_at	NIFU	-3.14	2.52E-23	5.58E-20	-2.18	-16.84	12q24.1
17	227670_at	ZNF75A	-8.18	2.91E-19	1.51E-16	-2.42	-16.78	16p13.11
18	AFFX-HUMGAPDH/M33197_M_at - HG-U133A	GAPD	2.88	1.83E-22	3.24E-19	2.18	16.74	12p13
19	AFFX-HUMGAPDH/M33197_M_at - HG-U133B	GAPD	2.83	2.01E-22	3.24E-19	2.17	16.67	12p13
20	208864_s_at	TXN	5.66	1.15E-16	1.63E-14	2.46	16.56	9q31
21	201417_at		25.91	2.14E-15	1.76E-13	2.66	16.45	
22	211787_s_at	EIF4A1	2.68	2.52E-20	2.03E-17	2.20	16.44	17p13
23	AFFX-HUMGAPDH/M33197_3_at - HG-U133A	GAPD	2.09	1.65E-23	4.49E-20	2.10	16.40	12p13
24	204215_at	MGC4175	-4.08	2.78E-21	3.07E-18	-2.13	-16.15	7q21.1-q21.2
25	233177_s_at	MR-1	4.18	1.49E-17	3.26E-15	2.28	16.10	2q35

Table 2.1-2.78

26	215785_s_at	CYFIP2	-7.76	1.13E-19	6.90E-17	-2.21	-16.09	5q34
27	224833_at	ETS1	-5.86	6.34E-21	6.60E-18	-2.14	-16.07	11q23.3
28	226454_at	LOC92979	-4.48	2.31E-18	8.34E-16	-2.34	-16.02	12q13.13
29	224710_at	RAB34	15.28	2.65E-15	2.12E-13	2.53	15.96	17q11.1
30	227261_at	KLF12	-9.62	4.26E-18	1.24E-15	-2.36	-15.89	13q22
31	201200_at	CREG	5.69	3.07E-17	5.43E-15	2.25	15.85	1q24
32	223287_s_at	FOXP1	-5.32	2.77E-18	9.63E-16	-2.31	-15.84	3p14.1
33	226611_s_at	p30	6.26	2.95E-15	2.29E-13	2.50	15.83	17p11.2
34	202252_at	RAB13	5.39	4.13E-16	4.63E-14	2.34	15.76	1q21.2
35	213572_s_at	SERPINB1	4.44	6.35E-16	6.47E-14	2.34	15.65	6p25
36	236301_at		-17.09	7.24E-18	1.89E-15	-2.31	-15.59	
37	229844_at		-6.47	8.95E-18	2.17E-15	-2.29	-15.50	
38	223276_at	NID67	17.02	1.93E-14	1.03E-12	2.59	15.43	5q33.1
39	225927_at		-2.96	2.95E-22	4.35E-19	-1.96	-15.34	
40	212268_at	SERPINB1	5.56	1.27E-15	1.13E-13	2.30	15.32	6p25
41	212590_at	RRAS2	-7.07	3.09E-18	1.01E-15	-2.15	-15.25	11p15.2
42	214615_at	P2RY10	-8.82	1.02E-17	2.39E-15	-2.21	-15.19	Xq21.1
43	226905_at		5.91	1.01E-19	6.41E-17	2.01	15.18	
44	44790_s_at	C13orf18	-53.54	5.66E-17	8.79E-15	-2.48	-15.18	13q14.11
45	228390_at		-30.85	4.40E-17	7.09E-15	-2.38	-15.17	
46	212386_at		-14.55	1.99E-17	3.91E-15	-2.25	-15.16	
47	212313_at	MGC29816	-6.00	2.99E-19	1.51E-16	-2.04	-15.13	8p21.2
48	231310_at		8.50	3.71E-14	1.78E-12	2.57	15.11	
49	204198_s_at	RUNX3	-9.42	2.17E-18	8.01E-16	-2.08	-15.01	1p36
50	219471_at	C13orf18	-36.72	7.61E-17	1.12E-14	-2.42	-15.01	13q14.11
2.56	AML_inv(16) versus CML							
#	affy Id	HUGO name	fc	p	q	stn	t	Map Location
1	201029_s_at	CD99	5.28	8.31E-26	6.27E-23	4.05	29.96	Xp22.32
2	206676_at	CEACAM8	-18.41	7.91E-34	3.73E-30	-3.07	-25.48	19q13.2
3	209771_x_at	CD24	-11.10	2.71E-35	5.12E-31	-2.72	-23.39	6q21
4	216379_x_at	KIAA1919	-12.05	1.34E-34	1.26E-30	-2.69	-23.09	6q22
5	212531_at	LCN2	-13.18	2.99E-34	1.88E-30	-2.62	-22.54	9q34
6	211657_at	CEACAM6	-10.24	1.70E-31	6.40E-28	-2.60	-21.92	19q13.2
7	203021_at	SLPI	-12.91	7.17E-29	1.50E-25	-2.69	-21.82	20q12
8	205513_at	TCN1	-17.23	6.44E-27	7.95E-24	-2.74	-21.24	11q11-q12
9	203757_s_at	CEACAM6	-13.09	5.93E-30	1.60E-26	-2.52	-21.12	19q13.2
10	205653_at	CTSG	-12.07	3.88E-29	9.15E-26	-2.46	-20.55	14q11.2
11	201061_s_at	STOM	-3.93	8.07E-28	1.52E-24	-2.50	-20.42	9q34.1
12	207802_at	SGP28	-234.23	6.12E-25	3.04E-22	-2.81	-20.00	6p12.3
13	205557_at	BPI	-5.69	1.57E-30	4.93E-27	-2.33	-19.94	20q11.23-q12
14	231688_at		-20.27	2.81E-26	2.78E-23	-2.50	-19.88	
15	210244_at	CAMP	-28.02	5.79E-26	4.98E-23	-2.47	-19.62	3p21.3

Table 2.1-2.78

16	209772_s_at	CD24	-26.63	2.57E-25	1.67E-22	-2.44	-19.22	6q21
17	266_s_at	CD24	-13.20	1.62E-27	2.78E-24	-2.25	-18.85	6q21
18	201669_s_at	MARCKS	-28.00	2.72E-24	1.28E-21	-2.48	-18.85	6q22.2
19	200832_s_at	SCD	-11.33	4.02E-25	2.26E-22	-2.36	-18.76	10q23-q24
20	203936_s_at	MMP9	-16.59	2.47E-25	1.67E-22	-2.30	-18.56	20q11.2-q13.1
21	200985_s_at	CD59	-20.26	5.19E-24	2.33E-21	-2.32	-18.13	11p13
22	209369_at	ANXA3	-21.05	8.29E-24	3.55E-21	-2.30	-17.96	4q13-q22
23	211275_s_at	GYG	-3.09	2.71E-27	4.27E-24	-2.11	-17.95	3q24-q25.1
24	224967_at	UGCG	-6.04	7.71E-26	6.06E-23	-2.15	-17.91	9q31
25	208440_at	LIN7A	-13.71	1.26E-24	6.10E-22	-2.17	-17.66	12q21
26	219281_at	MSRA	-3.32	4.19E-25	2.26E-22	-2.13	-17.60	8p23.1
27	210638_s_at	FBXO9	-3.69	1.04E-25	7.52E-23	-2.08	-17.45	6p12.3-p11.2
28	201554_x_at	GYG	-3.51	8.80E-27	9.23E-24	-2.04	-17.37	3q24-q25.1
29	200983_x_at	CD59	-18.36	6.37E-23	2.07E-20	-2.25	-17.36	11p13
30	207269_at	DEFA4	-7.01	5.39E-27	7.27E-24	-2.02	-17.35	8p23
31	226726_at	LOC129642	-9.24	3.65E-23	1.35E-20	-2.21	-17.34	2p25.2
32	204430_s_at	SLC2A5	-7.99	1.63E-23	6.67E-21	-2.18	-17.33	1p36.2
33	202018_s_at	LTF	-5.86	7.67E-26	6.06E-23	-2.02	-17.16	3q21-q23
34	221952_x_at	KIAA1393	-2.02	4.80E-27	6.97E-24	-1.99	-17.09	14q23.1
35	223423_at	GPCR1	-4.99	6.74E-27	7.95E-24	-1.98	-17.04	3q26.2-q27
36	227019_at		-4.83	7.23E-27	8.03E-24	-1.98	-17.01	
37	204411_at	KIAA0449	-14.85	4.39E-23	1.52E-20	-2.13	-16.96	1pter-q31.3
38	210254_at	MS4A3	-3.79	4.13E-25	2.26E-22	-2.00	-16.93	11q12
39	218795_at	ACP6	-7.90	8.05E-24	3.53E-21	-2.03	-16.69	1q21
40	208651_x_at	CD24	-8.67	1.47E-25	1.02E-22	-1.94	-16.56	6q21
41	208650_s_at	CD24	-12.15	3.52E-26	3.32E-23	-1.92	-16.52	6q21
42	205863_at	S100A12	-4.78	5.81E-26	4.98E-23	-1.91	-16.44	1q21
43	223471_at	RAB3IP	-5.01	3.24E-25	1.91E-22	-1.93	-16.42	
44	230006_s_at	DKFZp313A2432	-5.11	2.19E-22	6.66E-20	-2.06	-16.39	11p14.2
45	201060_x_at	STOM	-3.85	1.75E-23	6.90E-21	-1.96	-16.21	9q34.1
46	205786_s_at	ITGAM	-4.80	2.93E-25	1.84E-22	-1.89	-16.20	16p11.2
47	224707_at	ORF1-FL49	-8.23	6.32E-23	2.07E-20	-1.95	-16.02	5q31.3
48	227567_at		-5.08	3.13E-25	1.90E-22	-1.87	-16.01	
49	204174_at	ALOX5AP	-3.90	6.06E-25	3.04E-22	-1.87	-15.97	13q12
50	215806_x_at	TRGC2	-6.37	1.71E-23	6.87E-21	-1.90	-15.87	7p15
2.57	AML_Inv(16) versus normalBM							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	201029_s_at	CD99	3.51	1.24E-14	1.69E-10	3.43	19.01	Xp22.32
2	202018_s_at	LTF	-6.20	3.78E-11	2.00E-08	-2.84	-15.16	3q21-q23
3	226326_at		-2.99	3.81E-11	2.00E-08	-2.70	-14.53	
4	224975_at	NFIA	-10.75	4.86E-07	2.26E-05	-3.53	-13.50	1p31.3-p31.2
5	223769_x_at	HT036	-2.42	1.50E-09	3.01E-07	-2.60	-13.44	1p34.1
6	200832_s_at	SCD	-6.49	1.27E-07	8.06E-06	-3.05	-13.44	10q23-q24

Table 2.1-2.78

7	200665_s_at	SPARC	8.11	4.31E-13	9.82E-10	2.42	13.31	5q31.3-q32
8	205382_s_at	DF	6.51	7.01E-13	1.13E-09	2.30	12.79	19p13.3
9	235733_at		-2.92	1.74E-11	1.40E-08	-2.29	-12.77	
10	228716_at		-3.91	1.75E-09	3.31E-07	-2.44	-12.75	
11	214109_at	LRBA	-1.76	3.03E-13	9.82E-10	-2.17	-12.52	4q31.22-q31.23
12	224710_at	RAB34	5.38	8.67E-14	5.31E-10	2.13	12.43	17q11.1
13	201417_at		3.98	4.08E-13	9.82E-10	2.15	12.33	
14	225923_at		-2.35	4.67E-10	1.25E-07	-2.28	-12.31	
15	231310_at		5.26	1.17E-13	5.31E-10	2.11	12.30	
16	204285_s_at	PMAIP1	6.16	5.69E-13	1.11E-09	2.13	12.17	18q21.31
17	212531_at	LCN2	-12.00	3.08E-07	1.59E-05	-2.69	-12.01	9q34
18	227041_at		-3.26	8.30E-13	1.13E-09	-2.06	-11.91	
19	202561_at	TNKS	-2.60	3.52E-10	1.04E-07	-2.18	-11.88	8p23.1
20	223276_at	NID67	4.26	8.10E-13	1.13E-09	2.06	11.84	5q33.1
21	203582_s_at	RAB4A	2.77	3.35E-12	3.81E-09	2.05	11.79	1q42-q43
22	223044_at	SLC11A3	-18.63	1.59E-06	5.04E-05	-3.12	-11.76	2q32
23	219304_s_at	SCDGF-B	-2.75	4.36E-08	3.79E-06	-2.38	-11.76	11q22.3
24	225346_at	LOC80298	-2.75	1.28E-07	8.06E-06	-2.42	-11.57	12q24.1
25	218262_at	FLJ22318	-3.50	9.78E-08	6.68E-06	-2.39	-11.54	5q35.3
26	228983_at		-2.04	3.51E-08	3.39E-06	-2.29	-11.49	
27	201496_x_at	MYH11	13.80	9.16E-12	8.94E-09	2.05	11.41	16p13.13-p13.12
28	204976_s_at	AMMECR1	-6.54	1.67E-06	5.22E-05	-2.82	-11.26	Xq22.3
29	215111_s_at	TSC22	7.76	3.20E-11	1.90E-08	2.10	11.24	13q14
30	226726_at	LOC129642	-5.98	1.82E-06	5.58E-05	-2.83	-11.20	2p25.2
31	235359_at		4.69	2.65E-12	3.30E-09	1.93	11.16	
32	202747_s_at	ITM2A	5.89	1.23E-11	1.05E-08	1.99	11.16	Xq13.3-Xq21.2
33	202746_at	ITM2A	5.36	1.86E-11	1.42E-08	1.98	11.05	Xq13.3-Xq21.2
34	226806_s_at		-11.61	3.29E-06	8.53E-05	-3.06	-10.99	
35	204900_x_at	SAP30	6.58	2.72E-11	1.77E-08	1.99	10.99	4q34.1
36	212967_x_at	NAP1L1	1.48	4.93E-12	5.18E-09	1.89	10.97	12q21.1
37	201497_x_at	MYH11	18.74	5.42E-11	2.64E-08	2.04	10.93	16p13.13-p13.12
38	224976_at	NFIA	-5.30	2.48E-06	6.89E-05	-2.76	-10.85	1p31.3-p31.2
39	226301_at	dJ55C23.6	-3.71	1.62E-07	9.68E-06	-2.18	-10.68	6q22.3-q23.3
40	226120_at	TTC8	-3.02	4.46E-08	3.84E-06	-2.08	-10.65	14q31.3
41	226190_at		-3.22	4.64E-09	7.12E-07	-1.97	-10.62	
42	217846_at	QARS	1.72	2.69E-11	1.77E-08	1.83	10.57	3p21.3-p21.1
43	217988_at	HEI10	2.54	1.09E-11	9.93E-09	1.82	10.51	14q11.1
44	232098_at		-3.60	1.10E-07	7.28E-06	-2.09	-10.49	
45	208668_x_at	HMGN2	-1.52	1.44E-08	1.69E-06	-1.98	-10.47	1p36.1
46	225792_at		-4.61	8.15E-08	5.80E-06	-2.03	-10.32	
47	230988_at		-6.92	5.13E-06	1.15E-04	-2.83	-10.31	
48	213908_at		-3.71	4.03E-08	3.68E-06	-1.98	-10.30	
49	238389_s_at		4.02	3.20E-11	1.90E-08	1.75	10.11	
50	209045_at	XPNPEP1	1.91	6.75E-11	3.08E-08	1.75	10.11	10q25.3

Table 2.1-2.78

2.58	AML_inv(3) versus AML_komplext							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	222229_x_at		1.59	1.43E-12	2.58E-08	1.49	10.36	
2	206781_at	DNAJC4	2.26	7.27E-11	4.54E-07	1.37	9.35	11q13
3	208730_x_at	RAB2	2.22	1.23E-09	1.71E-06	1.38	9.00	8q12.1
4	200093_s_at - HG-U133B	HINT1	1.88	6.67E-10	1.71E-06	1.21	8.35	5q31.2
5	213682_at	NUP50	-1.96	7.52E-11	4.54E-07	-1.14	-8.23	22q13.31
6	227708_at	EEF1A1	2.34	1.67E-08	8.16E-06	1.30	8.20	6q14.1
7	208826_x_at	HINT1	1.52	5.20E-10	1.64E-06	1.14	8.05	5q31.2
8	201202_at	PCNA	-2.84	2.31E-10	1.05E-06	-1.10	-7.93	20pter-p12
9	209122_at	ADFP	-4.15	1.08E-09	1.71E-06	-1.12	-7.82	9p21.3
10	200700_s_at	KDELR2	-2.80	1.13E-09	1.71E-06	-1.09	-7.67	7p22.2
11	201377_at	NICE-4	-1.90	5.46E-10	1.64E-06	-1.06	-7.67	1q21.3
12	203538_at	CAMLG	2.07	4.91E-08	1.51E-05	1.20	7.65	5q23
13	205436_s_at	H2AFX	-3.79	2.79E-09	2.71E-06	-1.12	-7.64	11q23.2-q23.3
14	218883_s_at	FLJ23468	-2.56	8.92E-10	1.71E-06	-1.07	-7.63	4q35.1
15	200094_s_at - HG-U133A	EEF2	1.41	4.93E-09	3.72E-06	1.09	7.56	19pter-q12
16	201663_s_at	SMC4L1	-2.49	1.36E-09	1.76E-06	-1.06	-7.55	3q26.1
17	201386_s_at	DDX15	-1.79	9.01E-10	1.71E-06	-1.05	-7.53	4p15.3
18	222047_s_at	ARS2	-1.55	1.08E-09	1.71E-06	-1.04	-7.50	7q21
19	212491_s_at	DNAJC8	-1.75	2.35E-09	2.61E-06	-1.05	-7.47	1p35.2
20	206550_s_at	NUP155	-2.08	2.18E-09	2.61E-06	-1.04	-7.40	5p13.1
21	203421_at	PIG11	-6.24	1.66E-08	8.16E-06	-1.14	-7.30	11p11.2
22	212031_at	S164	-1.92	2.84E-09	2.71E-06	-1.02	-7.28	14q24.3
23	213008_at	FLJ10719	-2.96	2.45E-09	2.61E-06	-1.01	-7.25	15q25-q26
24	202580_x_at	FOXM1	-3.95	7.57E-09	4.72E-06	-1.05	-7.25	12p13
25	218115_at	ASF1B	-2.62	4.20E-09	3.55E-06	-1.02	-7.24	19p13.12
26	213088_s_at	DNAJC9	-2.44	7.48E-09	4.72E-06	-1.03	-7.18	10q22.2
27	213292_s_at	SNX13	-2.17	6.26E-09	4.35E-06	-1.01	-7.16	7p21.1
28	204695_at	CDC25A	-4.38	1.11E-08	6.26E-06	-1.03	-7.14	3p21
29	218585_s_at	RAMP	-3.20	1.41E-08	7.48E-06	-1.04	-7.12	
30	208715_at	LOC54499	-2.21	4.16E-09	3.55E-06	-0.99	-7.11	1q22-q25
31	201457_x_at	BUB3	-1.73	4.55E-09	3.57E-06	-0.99	-7.10	10q26
32	222680_s_at	RAMP	-2.06	4.32E-09	3.55E-06	-0.98	-7.10	
33	211950_at	RBAF600	-2.14	6.18E-09	4.35E-06	-0.99	-7.08	1p36.13
34	223157_at	MGC3232	2.00	4.48E-07	5.23E-05	1.18	7.07	4q12
35	215123_at		-3.06	7.02E-09	4.70E-06	-0.97	-6.98	
36	227165_at	C13orf3	-2.41	1.84E-08	8.51E-06	-1.01	-6.98	13q11
37	218350_s_at	GMNN	-2.41	1.04E-08	6.07E-06	-0.97	-6.93	6p22.1
38	202954_at	UBE2C	-3.17	3.02E-08	1.21E-05	-1.02	-6.91	20q13.11
39	232247_at	FLJ14855	-2.01	8.55E-09	5.15E-06	-0.96	-6.91	3p21.31
40	214141_x_at	SFRS7	-1.77	1.72E-08	8.17E-06	-0.98	-6.90	2p22.1
41	201680_x_at	ARS2	-1.59	1.17E-08	6.43E-06	-0.95	-6.82	7q21

Table 2.1-2.78

42	202413_s_at	USP1	-1.82	3.54E-08	1.31E-05	-0.97	-6.82	1p32.1-p31.3
43	209619_at	CD74	2.00	1.60E-07	2.89E-05	1.03	6.82	5q32
44	200094_s_at - HG-U133B	EEF2	1.39	4.08E-08	1.44E-05	0.98	6.81	19pter-q12
45	226123_at	LOC286180	-3.56	2.20E-08	9.47E-06	-0.96	-6.80	8q12.1
46	204709_s_at	KIF23	-4.17	6.32E-08	1.77E-05	-1.03	-6.80	15q22.31
47	210140_at	CST7	-4.76	5.60E-08	1.66E-05	-1.01	-6.78	20p11.21
48	210178_x_at	FUSIP1	-1.97	1.54E-08	7.94E-06	-0.94	-6.77	1p36.11
49	227056_at		3.40	1.85E-06	1.23E-04	1.20	6.72	
50	204023_at	RFC4	-2.23	1.88E-08	8.51E-06	-0.93	-6.70	3q27
2.59	AML_inv(3) versus AML_t(15;17)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	203948_s_at	MPO	-9.22	7.85E-20	8.48E-16	-3.33	-20.18	17q23.1
2	203949_at	MPO	-5.92	7.32E-21	1.58E-16	-3.19	-19.69	17q23.1
3	205382_s_at	DF	-12.00	3.95E-15	1.07E-11	-3.44	-18.83	19p13.3
4	212953_x_at	CALR	-4.97	5.32E-16	2.30E-12	-2.76	-16.36	19p13.3-p13.2
5	200654_at	P4HB	-3.54	5.30E-18	3.81E-14	-2.62	-16.13	17q25
6	224918_x_at	MGST1	-5.40	5.25E-17	2.83E-13	-2.49	-15.29	12p12.3-p12.1
7	231736_x_at	MGST1	-6.11	7.03E-16	2.53E-12	-2.51	-15.14	12p12.3-p12.1
8	214450_at	CTSW	-6.80	4.70E-14	1.02E-10	-2.44	-14.29	11q13.1
9	205624_at	CPA3	-18.38	6.13E-12	5.51E-09	-2.76	-14.18	3q21-q25
10	206871_at	ELA2	-5.26	1.18E-15	3.64E-12	-2.20	-13.53	19p13.3
11	211990_at	HLA-DPA1	12.46	4.97E-11	2.98E-08	2.67	13.52	6p21.3
12	38487_at	STAB1	-5.47	4.81E-13	6.92E-10	-2.24	-13.06	3p21.31
13	217716_s_at	SEC61A1	-2.52	1.00E-13	1.65E-10	-2.15	-12.88	3q21.3
14	214575_s_at	AZU1	-8.67	1.00E-13	1.65E-10	-2.12	-12.73	19p13.3
15	238022_at		-7.63	7.53E-13	9.07E-10	-2.12	-12.49	
16	208852_s_at	CANX	-3.04	3.58E-12	3.68E-09	-2.18	-12.48	5q35
17	221739_at	IL27w	-2.20	1.28E-14	3.06E-11	-2.02	-12.47	19p13.3
18	208689_s_at	RPN2	-2.59	1.07E-13	1.65E-10	-2.02	-12.26	20q12-q13.1
19	221004_s_at	ITM2C	-4.37	5.63E-14	1.11E-10	-1.99	-12.16	2q37
20	233072_at	KIAA1857	-9.87	1.26E-10	6.35E-08	-2.39	-12.10	9q34
21	210788_s_at	retSDR4	-2.78	4.14E-12	4.06E-09	-2.00	-11.71	14q22.3
22	206914_at	CRTAM	6.73	2.22E-11	1.60E-08	2.03	11.62	11q22-q23
23	211709_s_at	SCGF	-5.57	6.43E-13	8.68E-10	-1.91	-11.55	19q13.3
24	213716_s_at	SECTM1	10.56	1.74E-09	5.54E-07	2.25	11.11	17q25
25	227353_at	EVER2	5.13	2.92E-10	1.24E-07	2.00	11.00	17q25.3
26	209021_x_at	KIAA0652	-5.31	1.35E-11	1.12E-08	-1.84	-10.90	11p11.12
27	214797_s_at	PCTK3	5.81	2.43E-10	1.05E-07	1.95	10.87	1q31-q32
28	208730_x_at	RAB2	2.63	4.23E-10	1.72E-07	1.98	10.86	8q12.1
29	202487_s_at	H2AV	-2.35	7.56E-13	9.07E-10	-1.76	-10.82	7p13
30	203675_at	NUCB2	-3.45	1.59E-11	1.27E-08	-1.83	-10.81	11p15.1-p14
31	217225_x_at	LOC283820	-2.26	2.10E-12	2.26E-09	-1.77	-10.77	16p13.13

Table 2.1-2.78

32	200652_at	SSR2	-1.99	1.05E-12	1.19E-09	-1.73	-10.68	1q21-q23
33	209215_at	TETRAN	-3.46	4.99E-12	4.68E-09	-1.75	-10.63	4p16.3
34	229168_at	DKFZp434K0621	-4.90	5.86E-10	2.30E-07	-1.95	-10.53	5q35.3
35	209619_at	CD74	4.55	1.98E-11	1.47E-08	1.72	10.36	5q32
36	221253_s_at	MGC3178	-3.26	1.04E-10	5.78E-08	-1.78	-10.33	6p24.3
37	210140_at	CST7	-8.32	1.51E-09	5.06E-07	-1.98	-10.31	20p11.21
38	224839_s_at	GPT2	-6.24	6.83E-11	3.88E-08	-1.74	-10.23	16q12.1
39	217770_at	PIGT	-2.32	1.69E-11	1.30E-08	-1.68	-10.17	20q12-q13.12
40	205614_x_at	MST1	-9.35	3.11E-09	8.56E-07	-2.03	-10.12	3p21
41	209732_at	CLECSF2	29.15	1.41E-08	2.74E-06	2.22	10.02	12p13-p12
42	201004_at	SSR4	-2.56	2.78E-11	1.82E-08	-1.64	-9.95	Xq28
43	204897_at	PTGER4	5.27	1.51E-10	7.41E-08	1.68	9.90	5p13.1
44	201029_s_at	CD99	-1.81	1.13E-11	9.73E-09	-1.61	-9.89	Xp22.32
45	241696_at		3.13	3.64E-11	2.25E-08	1.62	9.81	
46	214789_x_at	SRP46	4.12	8.67E-10	3.28E-07	1.71	9.76	11q22
47	201825_s_at	CGI-49	-3.27	2.66E-11	1.79E-08	-1.57	-9.61	1q44
48	204150_at	STAB1	-5.48	2.26E-09	6.96E-07	-1.74	-9.57	3p21.31
49	241383_at		-4.21	2.75E-09	7.92E-07	-1.75	-9.55	
50	200068_s_at - HG-U133B	CANX	-1.65	2.98E-11	1.89E-08	-1.55	-9.52	5q35
2.60	AML_inv(3) versus AML_t(8;21)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	203949_at	MPO	-5.44	5.57E-18	1.52E-13	-2.29	-14.96	17q23.1
2	203948_s_at	MPO	-6.74	3.58E-14	4.89E-10	-1.89	-12.11	17q23.1
3	209122_at	ADFP	-3.38	1.03E-12	9.42E-09	-1.55	-10.15	9p21.3
4	228827_at		-92.61	4.57E-10	2.08E-06	-1.97	-10.03	
5	217963_s_at	NGFRAP1	34.31	1.80E-08	2.47E-05	2.15	9.83	Xq22.1
6	211709_s_at	SCGF	-4.29	8.01E-12	5.47E-08	-1.44	-9.45	19q13.3
7	211084_x_at	PRKCN	5.66	3.98E-09	9.88E-06	1.59	9.24	2p21
8	205529_s_at	CBFA2T1	-14.76	2.25E-09	6.83E-06	-1.74	-9.20	8q22
9	233955_x_at	HSPC195	5.01	2.80E-08	3.47E-05	1.80	9.19	5q31.3
10	207839_s_at	LOC51754	3.06	2.36E-10	1.29E-06	1.45	9.13	9p13.1
11	213716_s_at	SECTM1	4.93	3.75E-09	9.88E-06	1.55	9.11	17q25
12	229406_at		-12.12	1.70E-09	6.39E-06	-1.60	-9.09	
13	202887_s_at	RTP801	4.18	5.07E-08	4.62E-05	1.52	8.39	10pter-q26.12
14	205528_s_at	CBFA2T1	-27.75	1.41E-08	2.15E-05	-1.56	-8.32	8q22
15	212895_s_at	ABR	2.87	3.10E-08	3.53E-05	1.36	8.06	17p13.3
16	212423_at	FLJ90798	3.77	4.04E-08	4.42E-05	1.34	7.93	10q22.3
17	206871_at	ELA2	-4.45	1.87E-09	6.39E-06	-1.22	-7.88	19p13.3
18	217226_s_at	BA108L7.2	3.17	4.71E-08	4.62E-05	1.31	7.79	10q24.31
19	204494_s_at	DKFZP434H132	4.61	3.95E-07	1.37E-04	1.56	7.76	15q22.33
20	225010_at	D10S170	2.54	1.04E-08	1.77E-05	1.23	7.75	10q21
21	210150_s_at	LAMA5	-3.67	7.23E-09	1.52E-05	-1.23	-7.73	20q13.2-q13.3

Table 2.1-2.78

22	226865_at		9.73	5.70E-07	1.64E-04	1.64	7.68	
23	211728_s_at	HYAL3	-3.34	8.95E-09	1.75E-05	-1.22	-7.67	3p21.3
24	228058_at	LOC124220	-2.54	9.74E-09	1.77E-05	-1.20	-7.59	16p13.3
25	210613_s_at	SYNGR1	-2.97	4.40E-09	1.00E-05	-1.17	-7.58	22q13.1
26	233467_s_at	PHEMX	2.46	6.91E-08	5.05E-05	1.26	7.56	11p15.5
27	227276_at	TEM7R	3.51	3.09E-07	1.23E-04	1.39	7.55	10p12.1
28	233072_at	KIAA1857	-4.59	5.06E-08	4.62E-05	-1.28	-7.49	9q34
29	206478_at	KIAA0125	22.61	9.17E-07	1.95E-04	1.71	7.46	14q32.33
30	222996_s_at	HSPC195	4.19	7.29E-07	1.77E-04	1.52	7.46	5q31.3
31	235468_at		-6.55	8.20E-08	5.47E-05	-1.32	-7.42	
32	201243_s_at	ATP1B1	5.00	4.26E-07	1.42E-04	1.37	7.42	1q22-q25
33	204495_s_at	DKFZP434H132	5.13	9.12E-07	1.95E-04	1.53	7.37	15q22.33
34	205382_s_at	DF	-6.33	7.39E-08	5.05E-05	-1.26	-7.35	19p13.3
35	201281_at	ADRM1	-2.12	1.71E-08	2.45E-05	-1.16	-7.35	20q13.33
36	227853_at		2.46	5.80E-08	4.96E-05	1.18	7.30	
37	213908_at		4.51	5.12E-07	1.57E-04	1.34	7.30	
38	219183_s_at	PSCD4	2.35	2.77E-07	1.16E-04	1.26	7.27	22q12.3-q13.1
39	217975_at	LOC51186	14.36	1.13E-06	2.26E-04	1.51	7.26	Xq22.1
40	221773_at		3.52	2.17E-07	1.02E-04	1.24	7.24	
41	215051_x_at	AIF1	2.45	9.99E-08	6.07E-05	1.19	7.23	6p21.3
42	242845_at		-4.10	4.98E-08	4.62E-05	-1.17	-7.21	
43	218854_at	SART2	6.30	1.20E-06	2.34E-04	1.48	7.20	6q22
44	222955_s_at	HT011	-2.24	6.72E-08	5.05E-05	-1.19	-7.19	Xq26.1
45	201811_x_at	SH3BP5	8.59	1.30E-06	2.41E-04	1.46	7.15	3p24.3
46	203820_s_at	KOC1	3.81	9.22E-07	1.95E-04	1.36	7.15	7p11
47	201288_at	ARHGDIB	-1.41	1.29E-08	2.07E-05	-1.10	-7.15	12p12.3
48	210115_at	RPL39L	-8.57	2.10E-07	1.02E-04	-1.33	-7.12	3q27
49	204548_at	STAR	-7.93	1.56E-07	8.38E-05	-1.23	-7.08	8p11.2
50	202759_s_at	AKAP2	-3.83	2.73E-08	3.47E-05	-1.10	-7.08	9q31-q33
2.61	AML_inv(3) versus CLL							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	224838_at	FOXP1	-4.02	6.58E-27	1.18E-22	-2.84	-20.86	3p14.1
2	225927_at		-4.93	3.18E-26	2.84E-22	-2.77	-20.35	
3	218829_s_at	KIAA1416	-5.60	2.78E-22	1.66E-18	-2.62	-18.58	8q12.1
4	223514_at	CARD11	-23.95	4.73E-20	9.41E-17	-2.83	-18.46	7p22
5	226123_at	LOC286180	-8.20	5.40E-22	2.26E-18	-2.48	-17.74	8q12.1
6	243780_at		-36.23	6.53E-19	8.98E-16	-2.67	-17.20	
7	201030_x_at	LDHB	2.37	1.03E-21	3.06E-18	2.34	17.02	12p12.2-p12.1
8	218191_s_at	FLJ11240	-2.92	6.31E-22	2.26E-18	-2.30	-16.74	6q12
9	208091_s_at	DKFZP564K0822	-12.30	8.45E-19	1.08E-15	-2.46	-16.48	7p14.1
10	204215_at	MGC4175	-4.44	1.89E-21	4.82E-18	-2.23	-16.26	7q21.1-q21.2
11	226454_at	LOC92979	-4.79	2.68E-19	4.35E-16	-2.23	-15.72	12q13.13
12	212827_at	IGHM	-6.32	4.29E-21	9.59E-18	-2.14	-15.69	14q32.33

Table 2.1-2.78

13	214615_at	P2RY10	-8.85	1.09E-17	7.53E-15	-2.27	-15.22	Xq21.1
14	44790_s_at	C13orf18	-62.00	5.14E-17	2.24E-14	-2.48	-15.21	13q14.11
15	212590_at	RRAS2	-7.29	1.95E-18	2.18E-15	-2.18	-15.17	11p15.2
16	219471_at	C13orf18	-48.59	6.33E-17	2.46E-14	-2.47	-15.12	13q14.11
17	213564_x_at	LDHB	1.87	8.69E-18	6.22E-15	2.08	14.78	12p12.2-p12.1
18	228390_at		-19.22	5.90E-17	2.34E-14	-2.25	-14.76	
19	212313_at	MGC29816	-5.53	6.06E-19	8.98E-16	-2.04	-14.65	8p21.2
20	202880_s_at	PSCD1	-3.89	8.68E-20	1.55E-16	-2.00	-14.64	17q25
21	208456_s_at	RRAS2	-10.56	4.70E-18	4.42E-15	-2.08	-14.61	11p15.2
22	236280_at		-16.23	1.34E-16	4.52E-14	-2.26	-14.53	
23	211984_at		-3.69	2.88E-18	3.03E-15	-2.01	-14.33	
24	239287_at		-32.35	3.46E-16	9.36E-14	-2.34	-14.29	
25	201200_at	CREG	7.14	5.74E-12	3.00E-10	2.47	14.28	1q24
26	206337_at	CCR7	-15.17	8.46E-17	3.03E-14	-2.10	-14.19	17q12-q21.2
27	244261_at	IL28RA	-57.53	4.73E-16	1.21E-13	-2.28	-14.12	1p36.11
28	223287_s_at	FOXP1	-4.31	3.08E-18	3.06E-15	-1.94	-14.00	3p14.1
29	236301_at		-12.56	1.83E-18	2.18E-15	-1.93	-13.99	
30	229844_at		-4.57	4.68E-17	2.13E-14	-2.02	-13.98	
31	204674_at	LRMP	-6.49	4.58E-17	2.13E-14	-2.01	-13.96	12p12.1
32	226989_at	LOC285705	-5.23	1.57E-16	5.19E-14	-2.05	-13.89	5q15
33	229072_at		-18.08	3.66E-16	9.64E-14	-2.11	-13.87	
34	221778_at	KIAA1718	-4.22	5.36E-18	4.79E-15	-1.91	-13.76	7q33-q35
35	223391_at	SGPP1	-8.22	8.35E-18	6.22E-15	-1.91	-13.72	14q23.1
36	204951_at	ARHH	-4.12	1.66E-17	1.03E-14	-1.91	-13.65	4p13
37	202524_s_at	SPOCK2	-6.30	4.13E-17	2.11E-14	-1.94	-13.65	10pter-q25.3
38	206398_s_at	CD19	-12.84	5.18E-16	1.29E-13	-2.03	-13.57	16p11.2
39	41220_at	MSF	-2.09	1.30E-15	2.86E-13	-1.94	-13.56	17q25
40	205484_at	SIT	-17.73	1.69E-15	3.60E-13	-2.15	-13.49	9p13-p12
41	216095_x_at	MTMR1	-3.15	1.27E-17	8.45E-15	-1.85	-13.35	Xq28
42	201998_at	SIAT1	-6.44	4.75E-17	2.13E-14	-1.87	-13.33	3q27-q28
43	212579_at	KIAA0650	-4.10	4.42E-17	2.13E-14	-1.87	-13.31	18p11.31
44	209374_s_at	IGHM	-6.10	6.84E-18	5.82E-15	-1.80	-13.17	14q32.33
45	213309_at	PLCL2	-6.14	5.59E-17	2.29E-14	-1.84	-13.15	3p24.3
46	227193_at		-4.88	3.14E-17	1.70E-14	-1.82	-13.11	
47	227670_at	ZNF75A	-4.28	8.42E-18	6.22E-15	-1.79	-13.07	16p13.11
48	214786_at	MAP3K1	-5.45	8.29E-17	3.03E-14	-1.83	-13.06	5q11.2
49	236226_at		-25.93	4.17E-15	8.12E-13	-2.01	-12.96	
50	224837_at	FOXP1	-2.61	7.45E-18	6.06E-15	-1.76	-12.94	3p14.1
2.62	AML_inv(3) versus CML							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	212531_at	LCN2	-11.33	3.93E-33	7.80E-29	-2.84	-23.24	9q34
2	205557_at	BPI	-8.11	3.76E-29	2.49E-25	-2.63	-21.30	20q11.23-q12
3	204174_at	ALOX5AP	-9.82	6.03E-29	2.99E-25	-2.55	-20.60	13q12

Table 2.1-2.78

4	203021_at	SLPI	-9.44	9.41E-29	3.73E-25	-2.53	-20.43	20q12
5	210140_at	CST7	-7.08	1.29E-29	1.28E-25	-2.49	-20.33	20p11.21
6	206676_at	CEACAM8	-8.54	3.10E-28	8.78E-25	-2.45	-19.93	19q13.2
7	205513_at	TCN1	-12.10	1.81E-27	4.48E-24	-2.48	-19.84	11q11-q12
8	203757_s_at	CEACAM6	-9.79	1.39E-28	4.62E-25	-2.36	-19.30	19q13.2
9	207802_at	SGP28	-29.32	7.15E-25	7.89E-22	-2.50	-19.11	6p12.3
10	209772_s_at	CD24	-17.79	4.07E-25	5.38E-22	-2.39	-18.69	6q21
11	226789_at		-5.45	3.02E-27	5.99E-24	-2.29	-18.64	
12	214575_s_at	AZU1	-10.51	7.41E-27	1.34E-23	-2.25	-18.37	19p13.3
13	201554_x_at	GYG	-4.44	2.14E-27	4.73E-24	-2.24	-18.34	3q24-q25.1
14	210244_at	CAMP	-15.15	4.36E-26	7.22E-23	-2.21	-17.94	3p21.3
15	206871_at	ELA2	-6.00	3.94E-20	1.50E-17	-2.32	-17.70	19p13.3
16	225386_s_at	LOC92906	-8.21	5.64E-24	5.60E-21	-2.19	-17.55	2p22.2
17	206440_at	LIN7A	-16.13	5.02E-25	6.23E-22	-2.18	-17.52	12q21
18	203949_at	MPO	-5.20	9.71E-23	6.22E-20	-2.19	-17.37	17q23.1
19	203467_at	PMM1	-5.59	7.71E-26	1.18E-22	-2.10	-17.21	22q13.2
20	208308_s_at	GPI	-3.87	8.43E-24	7.61E-21	-2.13	-17.16	19q13.1
21	223423_at	GPCR1	-5.39	6.93E-25	7.89E-22	-2.06	-16.77	3q26.2-q27
22	212318_at	TRN-SR	-3.30	3.44E-25	4.88E-22	-2.04	-16.70	7q32.2
23	209369_at	ANXA3	-10.45	2.02E-23	1.67E-20	-2.05	-16.41	4q13-q22
24	217762_s_at	RAB31	-7.89	6.78E-24	6.41E-21	-2.02	-16.36	18p11.3
25	216379_x_at	KIAA1919	-6.15	1.94E-20	7.69E-18	-2.09	-16.33	6q22
26	204351_at	S100P	-5.29	3.11E-24	3.25E-21	-2.00	-16.31	4p16
27	211657_at	CEACAM6	-6.01	3.17E-22	1.91E-19	-2.02	-16.20	19q13.2
28	204411_at	KIAA0449	-11.88	3.63E-23	2.67E-20	-2.00	-16.04	1pter-q31.3
29	205863_at	S100A12	-5.50	3.22E-23	2.46E-20	-1.95	-15.85	1q21
30	205653_at	CTSG	-6.59	7.74E-23	5.30E-20	-1.95	-15.79	14q11.2
31	209771_x_at	CD24	-5.43	8.91E-19	2.21E-16	-2.05	-15.75	6q21
32	221952_x_at	KIAA1393	-2.40	2.83E-19	8.78E-17	-2.02	-15.69	14q23.1
33	219281_at	MSRA	-3.15	8.82E-24	7.62E-21	-1.92	-15.69	8p23.1
34	202487_s_at	H2AV	-2.86	3.79E-21	1.75E-18	-1.96	-15.64	7p13
35	208650_s_at	CD24	-7.56	2.92E-23	2.32E-20	-1.92	-15.62	6q21
36	200654_at	P4HB	-2.97	4.41E-17	6.29E-15	-2.09	-15.60	17q25
37	206656_s_at	C20orf3	-3.26	5.73E-23	4.06E-20	-1.85	-15.14	20p11.22-p11.21
38	207269_at	DEFA4	-6.47	1.92E-19	6.15E-17	-1.93	-15.14	8p23
39	210254_at	MS4A3	-4.96	7.30E-17	9.23E-15	-2.02	-15.10	11q12
40	219010_at	FLJ10901	-5.45	9.27E-23	6.14E-20	-1.85	-15.10	1q31.3
41	203948_s_at	MPO	-6.15	1.66E-21	8.91E-19	-1.86	-15.03	17q23.1
42	224707_at	ORF1-FL49	-6.35	4.75E-22	2.77E-19	-1.86	-15.00	5q31.3
43	204301_at	KIAA0711	-11.17	1.46E-20	6.06E-18	-1.94	-14.99	8p23.2
44	211275_s_at	GYG	-3.21	1.68E-20	6.83E-18	-1.86	-14.86	3q24-q25.1
45	236979_at		-4.04	1.79E-21	9.33E-19	-1.85	-14.83	
46	208651_x_at	CD24	-5.58	1.75E-22	1.09E-19	-1.81	-14.80	6q21
47	206851_at	RNASE3	-6.81	4.88E-22	2.77E-19	-1.81	-14.76	14q24-q31
48	218660_at	DYSF	-5.36	3.54E-21	1.67E-18	-1.82	-14.59	2p13.3-p13.1
49	217763_s_at	RAB31	-8.22	4.59E-21	2.07E-18	-1.82	-14.57	18p11.3

50	203936_s_at	MMP9	-9.33	2.43E-21	1.24E-18	-1.78	-14.45	20q11.2-q13.1
2.63	AML_inv(3) versus normalBM							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	225923_at		-2.50	2.61E-10	6.95E-07	-2.52	-12.56	
2	212531_at	LCN2	-10.31	5.31E-07	6.23E-05	-2.96	-12.01	9q34
3	202018_s_at	LTF	-4.47	3.71E-11	5.12E-07	-2.33	-11.96	3q21-q23
4	232098_at		-6.49	4.46E-09	4.79E-06	-2.34	-11.45	
5	218662_s_at	HCAP-G	-3.13	1.86E-08	8.49E-06	-2.37	-11.29	4p16-p15
6	223545_at	FANCD2	-2.57	5.47E-08	1.87E-05	-2.39	-11.13	3p26
7	226556_at		-2.92	7.16E-11	5.12E-07	-2.11	-10.96	
8	213292_s_at	SNX13	-2.90	3.38E-07	4.93E-05	-2.46	-10.85	7p21.1
9	225788_at	LOC88745	-1.50	1.22E-10	5.12E-07	-2.10	-10.85	6p21.1
10	209054_s_at	WHSC1	-2.56	6.09E-08	1.95E-05	-2.27	-10.71	4p16.3
11	218257_s_at	UGCGL1	-1.94	1.36E-10	5.12E-07	-2.01	-10.44	2q14.3
12	203535_at	S100A9	-3.26	1.39E-08	7.27E-06	-2.13	-10.43	1q21
13	208668_x_at	HMGN2	-1.66	6.58E-10	1.24E-06	-2.02	-10.34	1p36.1
14	212967_x_at	NAP1L1	1.53	2.78E-10	6.95E-07	1.97	10.19	12q21.1
15	228983_at		-2.03	5.91E-09	5.13E-06	-1.97	-9.92	
16	227708_at	EEF1A1	3.15	1.26E-09	1.81E-06	1.94	9.89	6q14.1
17	222430_s_at	HGRG8	2.23	4.23E-10	9.08E-07	1.90	9.86	14q12-21
18	203538_at	CAMLG	2.88	1.32E-09	1.81E-06	1.88	9.65	5q23
19	228566_at		-2.75	1.78E-06	1.39E-04	-2.22	-9.57	
20	219588_s_at	FLJ20311	-3.83	2.19E-06	1.53E-04	-2.23	-9.53	7q36.3
21	206871_at	ELA2	-5.73	5.98E-07	6.71E-05	-2.07	-9.46	19p13.3
22	235733_at		-2.62	1.05E-09	1.75E-06	-1.82	-9.43	
23	201988_s_at	CREBL2	-2.10	4.18E-09	4.79E-06	-1.84	-9.43	12p13
24	215111_s_at	TSC22	7.35	2.88E-08	1.14E-05	2.07	9.43	13q14
25	222606_at	FLJ10036	-1.77	2.46E-08	1.04E-05	-1.87	-9.33	15q22.2
26	218829_s_at	KIAA1416	-3.84	5.12E-06	2.40E-04	-2.28	-9.26	8q12.1
27	203755_at	BUB1B	-2.71	1.28E-06	1.09E-04	-2.05	-9.21	15q15
28	230988_at		-4.72	5.08E-06	2.40E-04	-2.24	-9.18	
29	225619_at	FLJ30046	-7.68	6.46E-06	2.71E-04	-2.30	-9.18	13q21.33
30	204976_s_at	AMMECR1	-3.62	2.33E-06	1.58E-04	-2.10	-9.14	Xq22.3
31	203746_s_at	HCCS	-1.77	4.91E-06	2.38E-04	-2.21	-9.12	Xp22.3
32	221030_s_at	DKFZP564B1162	-2.47	1.58E-07	3.31E-05	-1.88	-9.11	4q21.3
33	230044_at		-5.51	6.19E-06	2.66E-04	-2.25	-9.10	
34	227554_at		-2.51	4.95E-06	2.39E-04	-2.20	-9.09	
35	233701_at		-2.19	5.17E-07	6.12E-05	-1.94	-9.08	
36	203073_at	COG2	-1.99	7.77E-09	5.56E-06	-1.77	-9.07	1q42.13
37	203221_at	TLE1	-2.29	1.40E-08	7.27E-06	-1.78	-9.05	9q21.32
38	204767_s_at	FEN1	-2.16	6.84E-09	5.41E-06	-1.76	-9.04	11q12
39	219471_at	C13orf18	-6.25	1.45E-05	4.10E-04	-2.51	-8.97	13q14.11
40	203582_s_at	RAB4A	2.63	2.82E-09	3.53E-06	1.73	8.97	1q42-q43

41	235158_at	FLJ14803	-2.08	5.08E-09	4.93E-06	-1.75	-8.97	7q32.3
42	206845_s_at	RNF40	-2.14	7.49E-09	5.56E-06	-1.73	-8.92	16p11.2-p11.1
43	201858_s_at	PRG1	-2.04	1.62E-08	8.09E-06	-1.74	-8.87	10q22.1
44	214813_at	ZNF75	-2.32	2.97E-07	4.50E-05	-1.84	-8.84	Xq26.3
45	226190_at		-3.55	5.24E-09	4.93E-06	-1.70	-8.81	
46	226089_at	MGC23920	-2.09	6.08E-08	1.95E-05	-1.76	-8.79	3q13.33
47	205909_at	POLE2	-2.45	8.69E-07	8.65E-05	-1.88	-8.76	14q21-q22
48	228252_at	PIF1	-3.51	5.39E-06	2.45E-04	-2.05	-8.69	15q22.1
49	214575_s_at	AZU1	-7.76	2.88E-06	1.79E-04	-1.96	-8.69	19p13.3
50	210192_at	ATP8A1	-2.38	1.34E-07	2.96E-05	-1.76	-8.66	4p14-p12
2.64	AML_komplext versus AML_t(15;17)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	205382_s_at	DF	-7.84	1.62E-15	2.79E-12	-2.74	-17.32	19p13.3
2	212953_x_at	CALR	-3.21	1.30E-13	9.18E-11	-2.45	-15.03	19p13.3-p13.2
3	203948_s_at	MPO	-4.01	3.68E-19	4.69E-15	-2.02	-14.64	17q23.1
4	214450_at	CTSW	-6.67	6.70E-14	6.09E-11	-2.28	-14.52	11q13.1
5	38487_at	STAB1	-5.91	5.67E-13	2.67E-10	-2.18	-13.64	3p21.31
6	216032_s_at	SDBCAG84	-3.37	2.16E-14	2.29E-11	-2.03	-13.59	20pter-q12
7	208826_x_at	HINT1	-1.69	7.49E-18	4.77E-14	-1.76	-12.96	5q31.2
8	238022_at		-7.84	7.82E-13	3.55E-10	-1.99	-12.81	
9	213147_at	HOXA10	11.01	4.54E-15	5.75E-12	1.91	12.80	7p15-p14
10	200931_s_at	VCL	4.91	6.72E-16	1.71E-12	1.82	12.74	10q22.1-q23
11	209732_at	CLECSF2	35.32	4.46E-14	4.37E-11	2.04	12.46	12p13-p12
12	200654_at	P4HB	-2.34	2.10E-16	8.89E-13	-1.70	-12.36	17q25
13	207721_x_at	HINT1	-1.89	6.21E-16	1.71E-12	-1.57	-11.54	5q31.2
14	200047_s_at - HG-U133A	YY1	2.32	1.07E-15	2.27E-12	1.55	11.37	14q
15	203949_at	MPO	-2.48	1.75E-15	2.79E-12	-1.53	-11.23	17q23.1
16	200093_s_at - HG-U133B	HINT1	-1.89	2.93E-15	4.15E-12	-1.50	-11.06	5q31.2
17	201923_at	PRDX4	8.38	3.10E-13	1.80E-10	1.63	11.02	Xp22.13
18	204897_at	PTGER4	5.03	4.97E-15	5.75E-12	1.48	10.91	5p13.1
19	217225_x_at	LOC283820	-2.07	6.98E-12	1.85E-09	-1.59	-10.73	16p13.13
20	227353_at	EVER2	4.55	1.06E-13	7.94E-11	1.51	10.69	17q25.3
21	206847_s_at	HOXA7	4.94	9.60E-14	7.94E-11	1.47	10.53	7p15-p14
22	227999_at	LOC170394	3.30	1.56E-13	1.04E-10	1.41	10.21	10q26.3
23	202600_s_at	NRIP1	12.57	3.27E-12	9.68E-10	1.52	10.19	21q11.2
24	207375_s_at	IL15RA	5.82	1.33E-12	5.36E-10	1.46	10.16	10p15-p14
25	214789_x_at	SRP46	3.86	1.77E-13	1.13E-10	1.40	10.14	11q22
26	221004_s_at	ITM2C	-3.41	2.27E-13	1.38E-10	-1.40	-10.14	2q37
27	204150_at	STAB1	-6.71	1.26E-09	8.02E-08	-1.73	-10.06	3p21.31
28	200934_at	DEK	2.41	1.06E-13	7.94E-11	1.36	10.01	6p23
29	208892_s_at	DUSP6	6.46	1.35E-12	5.36E-10	1.39	9.84	12q22-q23

Table 2.1-2.78

30	202413_s_at	USP1	2.49	4.61E-13	2.37E-10	1.35	9.84	1p32.1-p31.3
31	217848_s_at	PP	3.96	1.63E-12	6.11E-10	1.38	9.78	10q11.1-q24
32	208891_at	DUSP6	6.82	9.06E-13	3.98E-10	1.36	9.77	12q22-q23
33	220798_x_at	FLJ11535	-3.66	2.63E-11	5.28E-09	-1.42	-9.75	19p13.3
34	224473_x_at	KIAA1813	2.33	9.97E-13	4.23E-10	1.36	9.75	10q24
35	225547_at		1.73	3.36E-13	1.86E-10	1.33	9.75	
36	200008_s_at - HG-U133A	GDI2	-2.39	1.53E-11	3.41E-09	-1.40	-9.74	10p15
37	238949_at	FLJ31951	8.00	5.50E-12	1.49E-09	1.41	9.71	5q33.3
38	203535_at	S100A9	7.92	3.22E-12	9.68E-10	1.38	9.68	1q21
39	210788_s_at	retSDR4	-2.19	8.24E-11	1.17E-08	-1.44	-9.67	14q22.3
40	226460_at	KIAA1450	3.63	1.79E-12	6.33E-10	1.35	9.66	4q32.1
41	200093_s_at - HG-U133A	HINT1	-1.69	5.55E-13	2.67E-10	-1.32	-9.63	5q31.2
42	225172_at	CRAMP1L	2.61	4.65E-13	2.37E-10	1.31	9.60	16p13.3
43	229693_at		-2.78	1.07E-10	1.42E-08	-1.42	-9.56	
44	203302_at	DCK	4.08	4.56E-12	1.30E-09	1.33	9.44	4q13.3-q21.1
45	200656_s_at	P4HB	-4.16	1.53E-09	9.31E-08	-1.51	-9.39	17q25
46	205033_s_at	DEFA1	5.34	2.50E-12	8.36E-10	1.30	9.37	8p23.2-p23.1
47	227308_x_at	SCYL1	4.60	1.47E-11	3.34E-09	1.35	9.36	
48	205663_at	PCBP3	-3.06	1.14E-10	1.44E-08	-1.37	-9.35	21q22.3
49	202599_s_at	NRIP1	8.20	2.13E-11	4.38E-09	1.36	9.31	21q11.2
50	221087_s_at	APOL3	3.50	4.58E-12	1.30E-09	1.29	9.29	22q13.1
2.65	AML_komplext versus AML_t(8;21)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	213147_at	HOXA10	7.91	8.54E-15	1.20E-10	1.70	12.02	7p15-p14
2	201920_at	SLC20A1	3.17	3.09E-14	2.18E-10	1.46	10.83	2q11-q14
3	206847_s_at	HOXA7	4.06	5.19E-13	1.46E-09	1.43	10.29	7p15-p14
4	222229_x_at		-1.45	5.56E-14	2.61E-10	-1.29	-9.90	
5	200833_s_at	RAP1B	2.26	3.79E-13	1.33E-09	1.27	9.62	12q14
6	228827_at		-24.12	6.82E-10	1.35E-07	-1.66	-9.62	
7	209523_at	TAF2	3.00	6.58E-13	1.55E-09	1.23	9.37	8q24.12
8	206940_s_at	POU4F1	-26.63	1.75E-09	2.40E-07	-1.69	-9.29	13q21.1-q22
9	224481_s_at	HECTD1	1.84	8.52E-13	1.72E-09	1.20	9.20	14q12
10	214651_s_at	HOXA9	111.95	1.42E-10	4.64E-08	1.55	9.15	7p15-p14
11	211423_s_at	SC5DL	2.73	2.78E-12	3.64E-09	1.21	9.12	11q23.3
12	217963_s_at	NGFRAP1	28.57	1.56E-10	4.76E-08	1.46	9.07	Xq22.1
13	209022_at	STAG2	2.17	1.59E-12	2.50E-09	1.18	9.04	Xq25
14	201807_at	VPS26	2.21	1.60E-12	2.50E-09	1.17	8.99	10q21.1
15	241706_at	LOC144402	5.97	4.36E-11	2.06E-08	1.27	8.98	12q11
16	206003_at	KIAA0635	2.44	2.87E-12	3.64E-09	1.16	8.90	4q12
17	212232_at	FNBP4	1.87	3.36E-12	3.64E-09	1.16	8.85	11p11.12
18	202406_s_at	TIAL1	1.77	3.16E-12	3.64E-09	1.15	8.84	10q

Table 2.1-2.78

19	203079_s_at	CUL2	2.44	3.64E-12	3.66E-09	1.15	8.83	10p11.21
20	212585_at	OSBPL8	2.34	5.76E-12	4.77E-09	1.16	8.80	12q14
21	201663_s_at	SMC4L1	3.00	4.61E-11	2.06E-08	1.22	8.78	3q26.1
22	218577_at	FLJ20331	2.34	4.62E-12	4.21E-09	1.15	8.77	1p31.1
23	227853_at		2.75	1.14E-11	8.46E-09	1.15	8.72	
24	222902_s_at	FLJ21144	1.96	4.78E-12	4.21E-09	1.13	8.70	1p34.1
25	211061_s_at	MGAT2	1.93	4.68E-11	2.06E-08	1.19	8.69	14q21
26	235753_at		6.97	3.87E-10	9.05E-08	1.36	8.68	
27	203949_at	MPO	-2.28	6.50E-12	5.09E-09	-1.13	-8.64	17q23.1
28	205529_s_at	CBFA2T1	-8.73	4.85E-09	4.90E-07	-1.44	-8.61	8q22
29	218236_s_at	PRKCN	7.50	2.70E-10	7.68E-08	1.26	8.60	2p21
30	201972_at	ATP6V1A1	2.49	3.96E-11	2.06E-08	1.16	8.57	3q13.2
31	226460_at	KIAA1450	2.94	3.24E-11	1.90E-08	1.14	8.53	4q32.1
32	212397_at	RDX	2.69	6.23E-11	2.58E-08	1.15	8.47	11q23
33	203320_at	LNK	2.62	1.00E-10	3.76E-08	1.16	8.45	12q24
34	211341_at	POU4F1	-75.39	1.11E-08	8.38E-07	-1.57	-8.44	13q21.1-q22
35	218754_at	FLJ23323	1.87	4.40E-11	2.06E-08	1.12	8.42	1p36.23
36	235521_at	HOXA3	7.65	7.60E-10	1.44E-07	1.31	8.42	7p15-p14
37	211746_x_at	PSMA1	1.68	1.55E-11	1.09E-08	1.09	8.39	11p15.1
38	203948_s_at	MPO	-2.93	5.41E-11	2.31E-08	-1.11	-8.36	17q23.1
39	212463_at		4.11	1.59E-10	4.76E-08	1.15	8.36	
40	218040_at	FLJ10330	2.14	2.71E-11	1.73E-08	1.10	8.36	1p13.2
41	201425_at	ALDH2	10.22	4.43E-10	9.67E-08	1.21	8.35	12q24.2
42	201377_at	NICE-4	2.04	2.58E-11	1.73E-08	1.09	8.31	1q21.3
43	215051_x_at	AIF1	2.38	3.60E-11	2.03E-08	1.08	8.25	6p21.3
44	217846_at	QARS	-1.58	3.17E-11	1.90E-08	-1.08	-8.25	3p21.3-p21.1
45	214700_x_at	DKFZP434D193	2.73	1.20E-10	4.22E-08	1.11	8.22	2q23.3
46	220936_s_at	H2AFJ	4.97	1.58E-10	4.76E-08	1.11	8.21	12p12
47	201994_at	MORF4L2	1.68	4.03E-11	2.06E-08	1.07	8.18	Xq22
48	202775_s_at	SFRS8	1.86	1.01E-10	3.76E-08	1.09	8.16	12q24.33
49	226545_at		7.60	8.73E-10	1.56E-07	1.19	8.16	
50	200934_at	DEK	1.96	4.59E-11	2.06E-08	1.06	8.13	6p23
2.66	AML_komplext versus CLL							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	224838_at	FOXP1	-4.30	3.70E-29	2.44E-25	-2.95	-23.50	3p14.1
2	209619_at	CD74	-3.42	2.95E-31	3.90E-27	-2.52	-21.05	5q32
3	212827_at	IGHM	-7.31	1.48E-21	2.98E-18	-2.26	-17.38	14q32.33
4	223514_at	CARD11	-14.56	1.18E-20	1.20E-17	-2.31	-17.28	7p22
5	243780_at		-24.21	3.92E-19	2.46E-16	-2.35	-16.68	
6	224837_at	FOXP1	-3.19	3.42E-21	4.51E-18	-2.15	-16.67	3p14.1
7	201200_at	CREG	7.30	1.82E-19	1.38E-16	2.21	16.42	1q24
8	225927_at		-3.37	3.61E-24	1.59E-20	-1.87	-15.65	
9	208091_s_at	DKFZP564K0822	-8.37	1.25E-18	6.60E-16	-2.10	-15.49	7p14.1

Table 2.1-2.78

10	208864_s_at	TXN	5.94	5.76E-18	2.11E-15	2.08	15.19	9q31
11	213911_s_at	H2AFZ	2.50	5.00E-19	3.00E-16	1.98	15.17	4q24
12	208456_s_at	RRAS2	-11.00	9.43E-18	2.89E-15	-2.11	-15.05	11p15.2
13	222680_s_at	RAMP	7.27	1.92E-16	3.20E-14	2.30	14.90	
14	212590_at	RRAS2	-6.68	2.26E-18	1.06E-15	-1.99	-14.89	11p15.2
15	217478_s_at	HLA-DMA	-3.42	4.04E-22	1.33E-18	-1.79	-14.80	6p21.3
16	AFFX-HUMGAPDH/M33197_3_at - HG-U133B	GAPD	2.43	1.37E-20	1.29E-17	1.81	14.65	12p13
17	203932_at	HLA-DMB	-5.71	1.88E-19	1.38E-16	-1.86	-14.64	6p21.3
18	223391_at	SGPP1	-9.69	7.57E-18	2.44E-15	-1.97	-14.58	14q23.1
19	229844_at		-5.13	2.40E-17	6.08E-15	-2.03	-14.57	
20	228390_at		-18.70	3.07E-17	7.35E-15	-2.03	-14.51	
21	41220_at	MSF	-2.30	2.04E-21	3.37E-18	-1.76	-14.51	17q25
22	223287_s_at	FOXP1	-3.96	2.15E-17	5.80E-15	-1.97	-14.37	3p14.1
23	209374_s_at	IGHM	-6.15	7.84E-18	2.46E-15	-1.92	-14.37	14q32.33
24	44790_s_at	C13orf18	-19.84	5.16E-17	1.06E-14	-2.01	-14.34	13q14.11
25	204670_x_at	HLA-DRB5	-2.82	9.35E-22	2.47E-18	-1.72	-14.30	6p21.3
26	201998_at	SIAT1	-7.78	4.13E-17	8.94E-15	-1.99	-14.30	3q27-q28
27	219471_at	C13orf18	-16.08	9.61E-17	1.74E-14	-2.01	-14.18	13q14.11
28	212313_at	MGC29816	-4.21	1.16E-17	3.25E-15	-1.87	-14.09	8p21.2
29	239287_at		-23.28	4.46E-16	6.68E-14	-2.19	-14.08	
30	226538_at		-4.00	8.19E-19	4.70E-16	-1.78	-14.06	
31	205105_at	MAN2A1	-2.98	6.57E-20	5.77E-17	-1.73	-14.02	5q21-q22
32	202880_s_at	PSCD1	-3.50	1.58E-21	2.98E-18	-1.68	-14.00	17q25
33	225246_at	STIM2	-4.68	2.80E-17	6.97E-15	-1.88	-13.97	4p15.2
34	AFFX-HUMGAPDH/M33197_3_at - HG-U133A	GAPD	2.13	8.11E-21	8.91E-18	1.68	13.93	12p13
35	208306_x_at	HLA-DRB4	-2.93	3.14E-21	4.51E-18	-1.66	-13.85	6p21.3
36	229072_at		-19.60	2.31E-16	3.77E-14	-1.97	-13.83	
37	213309_at	PLCL2	-6.43	8.19E-17	1.52E-14	-1.89	-13.79	3p24.3
38	214615_at	P2RY10	-6.31	1.04E-17	2.98E-15	-1.79	-13.76	Xq21.1
39	201263_at	TARS	4.89	9.13E-16	1.22E-13	2.01	13.75	5p13.2
40	209061_at	SULF2	-5.23	3.32E-17	7.64E-15	-1.82	-13.68	20q12-13.2
41	236301_at		-9.65	1.98E-18	9.68E-16	-1.71	-13.59	
42	224578_at	TD-60	2.90	2.39E-16	3.85E-14	1.86	13.59	1p36.13
43	204192_at	CD37	-4.73	2.24E-17	5.91E-15	-1.77	-13.54	19p13-q13.4
44	226635_at		-4.13	1.62E-16	2.78E-14	-1.84	-13.49	
45	206398_s_at	CD19	-13.04	3.63E-16	5.57E-14	-1.89	-13.48	16p11.2
46	236280_at		-10.91	7.32E-17	1.41E-14	-1.80	-13.48	
47	200853_at	H2AFZ	3.32	6.45E-17	1.27E-14	1.78	13.47	4q24
48	209312_x_at	HLA-DRB1	-3.04	7.56E-21	8.91E-18	-1.61	-13.47	6p21.3
49	202503_s_at	KIAA0101	29.94	5.71E-15	5.98E-13	2.21	13.45	15q22.1
50	212589_at	RRAS2	-7.40	1.02E-17	2.98E-15	-1.72	-13.44	11p15.2

Table 2.1-2.78

2.67	AML_komplext versus CML							
#	affy Id	HUGO name	fc	p	q	stn	t	Map Location
1	210244_at	CAMP	-14.07	5.78E-26	4.95E-22	-2.17	-18.39	3p21.3
2	212531_at	LCN2	-5.21	9.13E-27	1.56E-22	-1.81	-16.35	9q34
3	203936_s_at	MMP9	-9.17	2.25E-25	1.21E-21	-1.82	-16.22	20q11.2-q13.1
4	209772_s_at	CD24	-7.30	1.76E-24	6.01E-21	-1.79	-15.83	6q21
5	207802_at	SGP28	-11.06	2.83E-25	1.21E-21	-1.73	-15.58	6p12.3
6	205557_at	BPI	-3.43	6.31E-24	1.80E-20	-1.65	-14.88	20q11.23-q12
7	206676_at	CEACAM8	-3.92	2.68E-23	6.55E-20	-1.60	-14.41	19q13.2
8	203021_at	SLPI	-4.25	4.98E-23	1.07E-19	-1.53	-13.88	20q12
9	214575_s_at	AZU1	-4.15	7.83E-21	1.22E-17	-1.43	-12.94	19p13.3
10	204971_at	CSTA	-3.29	2.59E-21	4.93E-18	-1.42	-12.91	3q21
11	219281_at	MSRA	-2.58	6.56E-21	1.12E-17	-1.39	-12.67	8p23.1
12	208699_x_at	TKT	-2.69	1.40E-20	1.99E-17	-1.39	-12.62	3p14.3
13	206440_at	LIN7A	-4.02	2.43E-20	2.97E-17	-1.39	-12.58	12q21
14	208650_s_at	CD24	-3.98	1.86E-20	2.45E-17	-1.37	-12.45	6q21
15	266_s_at	CD24	-3.78	3.52E-20	4.02E-17	-1.35	-12.29	6q21
16	207384_at	PGLYRP	-10.11	2.89E-17	1.98E-14	-1.46	-12.16	19q13.2-q13.3
17	216379_x_at	KIAA1919	-3.20	2.34E-18	2.00E-15	-1.36	-12.07	6q22
18	208651_x_at	CD24	-3.50	1.20E-19	1.29E-16	-1.32	-12.02	6q21
19	218454_at	FLJ22662	-4.49	3.53E-19	3.56E-16	-1.31	-11.85	12p13.1
20	208645_s_at	RPS14	-1.46	9.23E-19	8.31E-16	-1.31	-11.81	5q31-q33
21	206697_s_at	HP	-4.56	2.66E-18	2.16E-15	-1.31	-11.70	16q22.1
22	223423_at	GPCR1	-2.95	8.62E-19	8.19E-16	-1.29	-11.70	3q26.2-q27
23	207269_at	DEFA4	-3.21	6.18E-18	4.81E-15	-1.29	-11.57	8p23
24	209771_x_at	CD24	-3.01	5.56E-17	3.66E-14	-1.32	-11.53	6q21
25	203079_s_at	CUL2	2.94	1.33E-14	3.05E-12	1.38	11.18	10p11.21
26	227929_at		-5.70	1.44E-16	6.68E-14	-1.27	-11.11	
27	236979_at		-2.76	1.06E-17	7.88E-15	-1.22	-11.09	
28	224573_at	MGC49942	-2.08	1.12E-17	7.96E-15	-1.22	-11.08	17p13.2
29	211890_x_at	CAPN3	-7.57	2.59E-16	1.08E-13	-1.27	-11.04	15q15.1-q21.1
30	205627_at	CDA	-5.33	1.09E-16	5.69E-14	-1.25	-11.02	1p36.2-p35
31	203757_s_at	CEACAM6	-3.41	6.36E-17	3.75E-14	-1.23	-11.01	19q13.2
32	212586_at	ARTS-1	-2.88	1.29E-16	6.28E-14	-1.24	-11.00	5q14.3
33	208700_s_at	TKT	-2.15	5.99E-17	3.74E-14	-1.23	-10.99	3p14.3
34	224818_at		-3.33	6.12E-17	3.74E-14	-1.21	-10.85	
35	200654_at	P4HB	-1.96	1.54E-15	5.50E-13	-1.25	-10.83	17q25
36	205863_at	S100A12	-3.12	9.34E-17	5.18E-14	-1.21	-10.82	1q21
37	208470_s_at	HPR	-9.47	3.83E-15	1.18E-12	-1.31	-10.79	16q22.1
38	223894_s_at	FTS	-3.10	1.11E-16	5.69E-14	-1.20	-10.77	16q12.1
39	218251_at	STRAIT11499	-2.90	6.36E-16	2.47E-13	-1.23	-10.71	Xp11.4
40	206515_at	CYP4F3	-6.88	1.87E-16	8.20E-14	-1.19	-10.65	19p13.2
41	205653_at	CTSG	-2.96	1.54E-16	6.94E-14	-1.18	-10.62	14q11.2
42	220001_at	PADI4	-5.66	9.87E-16	3.67E-13	-1.20	-10.56	1p36.13

Table 2.1-2.78

43	201904_s_at	HYA22	-3.37	1.40E-16	6.63E-14	-1.17	-10.55	3p21.3
44	201029_s_at	CD99	3.55	1.08E-12	1.08E-10	1.44	10.54	Xp22.32
45	214523_at	CEBPE	-4.50	2.13E-15	7.13E-13	-1.22	-10.53	14q11.2
46	205538_at	CORO2A	-3.25	2.48E-16	1.06E-13	-1.17	-10.52	9q22.3
47	219010_at	FLJ10901	-2.61	1.13E-16	5.69E-14	-1.16	-10.52	1q31.3
48	202442_at	AP3S1	-2.09	9.38E-17	5.18E-14	-1.15	-10.51	5q22
49	206871_at	ELA2	-2.76	2.09E-14	4.40E-12	-1.24	-10.48	19p13.3
50	212783_at	RBBP6	2.67	1.91E-13	2.70E-11	1.31	10.46	16p12-p11.2
2.68	AML_komplext versus normalBM							
#	affy Id	HUGO name	fc	p	q	stn	t	Map Location
1	201595_s_at	HT010	2.39	1.81E-14	4.80E-10	1.86	11.99	2q32.1
2	201437_s_at	EIF4E	3.61	6.14E-13	8.17E-09	1.58	10.32	4q21-q25
3	201830_s_at	NET1	5.96	4.48E-12	1.52E-08	1.66	10.31	10p15
4	217812_at	HGRG8	2.09	5.57E-12	1.52E-08	1.56	10.08	14q12-21
5	210396_s_at		2.70	2.53E-12	1.35E-08	1.55	10.03	
6	216652_s_at		2.30	2.24E-12	1.35E-08	1.53	9.99	
7	202265_at	BMI1	4.75	6.27E-12	1.52E-08	1.53	9.85	10p11.23
8	200040_at - HG-U133A	KHDRBS1	1.63	2.38E-12	1.35E-08	1.50	9.84	1p32
9	200071_at - HG-U133A	SPF30	2.31	3.41E-12	1.51E-08	1.49	9.78	10q23
10	201560_at	CLIC4	4.23	6.02E-12	1.52E-08	1.51	9.74	1p36.11
11	218649_x_at	SDCCAG1	2.12	7.76E-12	1.57E-08	1.49	9.69	14q22
12	201994_at	MORF4L2	1.69	8.49E-12	1.57E-08	1.48	9.66	Xq22
13	222035_s_at	PAPOLA	2.26	8.37E-12	1.57E-08	1.48	9.66	14q32.31
14	212531_at	LCN2	-4.74	2.67E-07	1.94E-05	-1.78	-9.61	9q34
15	201263_at	TARS	2.47	5.20E-12	1.52E-08	1.47	9.60	5p13.2
16	201699_at	PSMC6	2.37	2.61E-11	3.16E-08	1.46	9.44	14q22.1
17	209388_at	PAPOLA	2.53	8.83E-12	1.57E-08	1.44	9.44	14q32.31
18	209806_at	HIST1H2BK	4.07	2.52E-11	3.16E-08	1.48	9.44	6p21.33
19	202018_s_at	LTF	-2.61	4.60E-10	1.97E-07	-1.50	-9.42	3q21-q23
20	208645_s_at	RPS14	-1.41	4.18E-09	8.99E-07	-1.54	-9.39	5q31-q33
21	214290_s_at	HIST2H2AA	5.84	1.36E-11	2.27E-08	1.43	9.37	1q21.2
22	211069_s_at	UBL1	2.06	2.21E-11	3.16E-08	1.44	9.31	2q33
23	201593_s_at	HT010	2.54	1.80E-10	1.09E-07	1.44	9.21	2q32.1
24	218224_at	PNMA1	3.91	6.10E-11	5.21E-08	1.46	9.21	14q24.1
25	200047_s_at - HG-U133A	YY1	1.89	1.23E-10	8.17E-08	1.42	9.13	14q
26	222430_s_at	HGRG8	2.43	1.98E-11	3.11E-08	1.39	9.13	14q12-21
27	201548_s_at	PLU-1	2.34	8.25E-11	6.25E-08	1.40	9.10	1q32.1
28	201077_s_at	NHP2L1	1.62	2.32E-11	3.16E-08	1.39	9.09	22q13.2-q13.31
29	218280_x_at	HIST2H2AA	6.41	2.92E-11	3.36E-08	1.39	9.09	1q21.2
30	209732_at	CLECSF2	4.12	3.03E-11	3.36E-08	1.39	9.07	12p13-p12
31	208843_s_at	GORASP2	2.16	2.55E-11	3.16E-08	1.38	9.05	2p24.3-q21.3

Table 2.1-2.78

32	201196_s_at	AMD1	2.10	2.68E-10	1.43E-07	1.40	8.96	6q21-q22
33	218823_s_at	FLJ20038	2.63	8.45E-11	6.25E-08	1.39	8.94	8p21.1
34	218582_at	FLJ20445	2.37	4.28E-11	4.25E-08	1.37	8.93	10q23.32
35	201917_s_at	FLJ10618	3.25	4.02E-11	4.25E-08	1.36	8.90	3q23
36	202824_s_at	TCEB1	2.12	4.31E-11	4.25E-08	1.35	8.88	8q13.3
37	218478_s_at	DKFZp434E2220	2.76	5.50E-11	4.88E-08	1.35	8.86	12q24.31
38	229269_x_at	ISYNA1	3.54	5.27E-11	4.88E-08	1.35	8.85	19p13.11
39	204299_at	FUSIP1	3.12	5.39E-11	4.88E-08	1.35	8.83	1p36.11
40	202467_s_at	TRIP15	1.95	5.60E-10	2.13E-07	1.38	8.82	15q21.2
41	209122_at	ADFP	5.68	1.40E-10	8.87E-08	1.38	8.81	9p21.3
42	209186_at	ATP2A2	1.86	6.44E-11	5.21E-08	1.34	8.77	12q23-q24.1
43	203582_s_at	RAB4A	2.83	6.47E-11	5.21E-08	1.34	8.76	1q42-q43
44	203177_x_at	TFAM	2.72	6.85E-11	5.36E-08	1.33	8.73	10q21
45	208546_x_at	HIST1H2BH	5.44	1.04E-10	7.48E-08	1.34	8.72	6p21.3
46	214651_s_at	HOXA9	16.40	4.99E-10	2.01E-07	1.45	8.66	7p15-p14
47	204203_at	CEBPG	2.89	1.39E-10	8.87E-08	1.33	8.63	19q13.11
48	215009_s_at		3.30	1.23E-10	8.17E-08	1.31	8.58	
49	218936_s_at	HSPC128	2.01	1.89E-10	1.10E-07	1.31	8.56	12q21.31
50	222000_at		2.21	1.21E-10	8.17E-08	1.30	8.54	
2.69	AML_t(15;17) versus AML_t(8;21)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	209732_at	CLECSF2	-31.87	6.61E-16	1.83E-11	-3.41	-18.50	12p13-p12
2	214450_at	CTSW	32.70	1.75E-13	8.07E-10	3.62	17.85	11q13.1
3	38487_at	STAB1	23.73	4.75E-13	1.20E-09	3.30	16.70	3p21.31
4	211990_at	HLA-DPA1	-11.38	8.43E-15	1.17E-10	-2.54	-15.15	6p21.3
5	212509_s_at		10.56	1.02E-10	8.07E-08	2.39	12.28	
6	221004_s_at	ITM2C	3.38	3.94E-13	1.20E-09	1.92	12.13	2q37
7	217478_s_at	HLA-DMA	-5.37	1.31E-13	8.07E-10	-1.90	-12.10	6p21.3
8	212953_x_at	CALR	2.46	4.33E-13	1.20E-09	1.86	11.84	19p13.3-p13.2
9	224839_s_at	GPT2	9.84	6.52E-11	6.28E-08	2.10	11.80	16q12.1
10	204150_at	STAB1	26.03	3.22E-10	1.88E-07	2.39	11.71	3p21.31
11	226878_at		-5.22	3.86E-12	7.65E-09	-1.95	-11.66	
12	205663_at	PCBP3	4.49	1.54E-11	2.38E-08	1.95	11.65	21q22.3
13	201596_x_at	KRT18	23.76	3.19E-10	1.88E-07	2.32	11.63	12q13
14	204316_at	RGS10	-2.58	2.53E-13	8.78E-10	-1.78	-11.47	10q25
15	205349_at	GNA15	3.44	3.85E-11	4.45E-08	1.90	11.27	19p13.3
16	211991_s_at	HLA-DPA1	-17.13	2.84E-11	3.58E-08	-1.96	-11.15	6p21.3
17	208689_s_at	RPN2	1.81	1.12E-13	8.07E-10	1.61	10.80	20q12-q13.1
18	209619_at	CD74	-4.53	1.48E-13	8.07E-10	-1.62	-10.79	5q32
19	200986_at	SERPING1	10.67	1.48E-09	6.06E-07	2.04	10.51	11q12-q13.1
20	208826_x_at	HINT1	1.43	2.32E-13	8.78E-10	1.56	10.48	5q31.2
21	227326_at		5.21	3.26E-10	1.88E-07	1.81	10.47	
22	204319_s_at	RGS10	-5.48	8.04E-11	7.19E-08	-1.76	-10.34	10q25

Table 2.1-2.78

23	209312_x_at	HLA-DRB1	-6.71	1.16E-11	1.89E-08	-1.63	-10.33	6p21.3
24	201522_x_at	SNRPN	-3.69	5.83E-13	1.35E-09	-1.55	-10.31	15q12
25	211474_s_at	SERPINB6	-5.66	8.59E-11	7.28E-08	-1.73	-10.26	6p25
26	217716_s_at	SEC61A1	1.98	7.38E-12	1.36E-08	1.57	10.18	3q21.3
27	228113_at	STAT3	-4.67	2.42E-11	3.20E-08	-1.62	-10.17	17q21
28	200953_s_at	CCND2	2.76	4.76E-10	2.49E-07	1.73	10.12	12p13
29	228827_at		-103.40	4.47E-10	2.43E-07	-1.98	-10.04	
30	207721_x_at	HINT1	1.57	1.19E-12	2.54E-09	1.48	9.94	5q31.2
31	208306_x_at	HLA-DRB4	-6.81	4.41E-11	4.89E-08	-1.57	-9.88	6p21.3
32	227353_at	EVER2	-3.90	1.85E-11	2.70E-08	-1.53	-9.83	17q25.3
33	201137_s_at	HLA-DPB1	-12.31	4.76E-10	2.49E-07	-1.76	-9.82	6p21.3
34	208852_s_at	CANX	2.25	8.79E-11	7.28E-08	1.55	9.79	5q35
35	238022_at		4.12	1.01E-11	1.76E-08	1.47	9.70	
36	201923_at	PRDX4	-6.62	1.94E-10	1.38E-07	-1.60	-9.69	Xp22.13
37	218795_at	ACP6	-2.77	4.94E-11	5.27E-08	-1.50	-9.56	1q21
38	206940_s_at	POU4F1	-45.36	1.38E-09	5.89E-07	-1.87	-9.48	13q21.1-q22
39	205614_x_at	MST1	6.64	5.11E-09	1.59E-06	1.73	9.46	3p21
40	223321_s_at	FGFRL1	4.08	3.37E-09	1.17E-06	1.65	9.40	4p16
41	205771_s_at	AKAP7	-5.88	1.70E-10	1.28E-07	-1.50	-9.39	6q23
42	215193_x_at	HLA-DRB1	-6.64	5.32E-11	5.46E-08	-1.45	-9.35	6p21.3
43	222307_at	LOC282997	-2.74	3.08E-11	3.71E-08	-1.43	-9.34	10q25.2
44	55093_at	CSGlcA-T	1.90	3.36E-10	1.90E-07	1.49	9.33	7q36.1
45	201952_at	ALCAM	4.60	2.47E-09	9.13E-07	1.58	9.27	3q13.1
46	201136_at	PLP2	2.92	7.82E-11	7.19E-08	1.42	9.25	Xp11.23
47	221865_at	DKFZp547P234	-3.09	8.93E-11	7.28E-08	-1.43	-9.21	9q33.1
48	205529_s_at	CBFA2T1	-14.51	2.28E-09	8.69E-07	-1.73	-9.18	8q22
49	224356_x_at	MS4A6A	-6.39	9.01E-10	4.23E-07	-1.55	-9.18	11q12.1
50	202732_at	PKIG	2.71	2.63E-09	9.36E-07	1.55	9.17	20q12-q13.1
2.70	AML_t(15;17) versus CLL							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	203949_at	MPO	185.37	3.80E-18	5.71E-16	6.90	32.46	17q23.1
2	211990_at	HLA-DPA1	-14.20	1.95E-31	3.19E-27	-4.06	-29.46	6p21.3
3	224838_at	FOXP1	-8.40	7.79E-29	2.55E-25	-4.12	-28.94	3p14.1
4	203948_s_at	MPO	410.53	1.27E-16	1.07E-14	5.88	26.98	17q23.1
5	208306_x_at	HLA-DRB4	-12.53	7.83E-31	5.38E-27	-3.49	-25.84	6p21.3
6	209619_at	CD74	-7.79	6.21E-30	2.54E-26	-3.33	-24.77	5q32
7	204670_x_at	HLA-DRB5	-9.72	9.86E-31	5.38E-27	-3.26	-24.39	6p21.3
8	200654_at	P4HB	5.99	3.09E-17	3.24E-15	4.07	24.03	17q25
9	226905_at		8.10	1.11E-26	2.27E-23	3.30	23.99	
10	206871_at	ELA2	210.99	1.41E-15	8.83E-14	4.95	23.57	19p13.3
11	206111_at	RNASE2	31.85	4.97E-16	3.48E-14	4.26	23.20	14q24-q31
12	224918_x_at	MGST1	44.95	9.91E-16	6.44E-14	4.40	23.07	12p12.3-p12.1

Table 2.1-2.78

13	217478_s_at	HLA-DMA	-13.59	1.09E-24	1.99E-21	-3.30	-22.98	6p21.3
14	209312_x_at	HLA-DRB1	-10.89	2.87E-28	7.83E-25	-3.06	-22.70	6p21.3
15	41220_at	MSF	-2.94	3.87E-27	9.05E-24	-2.86	-21.25	17q25
16	34210_at	CDW52	-66.18	7.63E-22	6.25E-19	-3.26	-21.11	1p36
17	212827_at	IGHM	-44.65	1.50E-21	1.07E-18	-3.34	-21.02	14q32.33
18	208689_s_at	RPN2	3.43	2.19E-19	5.96E-17	3.08	20.83	20q12-q13.1
19	231736_x_at	MGST1	44.46	1.11E-14	5.11E-13	4.05	20.63	12p12.3-p12.1
20	207168_s_at	H2AFY	3.54	2.09E-19	5.90E-17	3.03	20.56	5q31.3-q32
21	205382_s_at	DF	33.58	4.18E-15	2.26E-13	3.65	20.34	19p13.3
22	224833_at	ETS1	-22.25	2.82E-21	1.77E-18	-3.08	-20.14	11q23.3
23	200650_s_at	LDHA	3.22	1.52E-24	2.49E-21	2.70	19.86	11p15.4
24	224837_at	FOXP1	-4.89	2.41E-23	3.59E-20	-2.71	-19.48	3p14.1
25	AFFX-HUMGAPDH/M33197_M_at - HG-U133A	GAPD	3.56	3.26E-20	1.41E-17	2.77	19.41	12p13
26	221004_s_at	ITM2C	54.89	4.37E-14	1.58E-12	3.82	19.24	2q37
27	223514_at	CARD11	-52.28	4.33E-20	1.77E-17	-3.11	-19.07	7p22
28	212953_x_at	CALR	5.80	3.56E-14	1.34E-12	3.56	18.91	19p13.3-p13.2
29	200999_s_at	CKAP4	-9.47	4.73E-22	4.30E-19	-2.65	-18.78	12q24.11
30	221739_at	IL27w	2.89	4.22E-18	6.17E-16	2.72	18.50	19p13.3
31	224482_s_at	RAB11-FIP4	-24.78	4.58E-20	1.82E-17	-2.82	-18.47	
32	201029_s_at	CD99	2.70	4.12E-18	6.08E-16	2.69	18.34	Xp22.32
33	202880_s_at	PSCD1	-4.54	3.63E-23	4.95E-20	-2.40	-17.75	17q25
34	202863_at	SP100	-5.41	2.35E-21	1.54E-18	-2.48	-17.72	2q37.1
35	212400_at		-6.06	1.26E-21	9.34E-19	-2.46	-17.71	
36	203932_at	HLA-DMB	-12.97	1.01E-19	3.11E-17	-2.64	-17.69	6p21.3
37	243780_at		-111.12	5.14E-19	1.14E-16	-2.86	-17.62	
38	204215_at	MGC4175	-5.59	1.43E-22	1.67E-19	-2.40	-17.62	7q21.1-q21.2
39	AFFX-HUMGAPDH/M33197_M_at - HG-U133B	GAPD	3.68	3.99E-17	4.01E-15	2.61	17.58	12p13
40	215193_x_at	HLA-DRB1	-10.91	4.12E-23	5.18E-20	-2.37	-17.54	6p21.3
41	208091_s_at	DKFZP564K0822	-26.27	4.79E-19	1.07E-16	-2.76	-17.53	7p14.1
42	209374_s_at	IGHM	-37.97	5.69E-19	1.22E-16	-2.80	-17.51	14q32.33
43	201137_s_at	HLA-DPB1	-18.09	2.10E-19	5.90E-17	-2.63	-17.45	6p21.3
44	214450_at	CTSW	21.74	1.51E-13	4.37E-12	3.25	17.43	11q13.1
45	AFFX-HUMGAPDH/M33197_5_at - HG-U133A	GAPD	5.33	4.11E-15	2.25E-13	2.78	17.35	12p13
46	236248_x_at		-10.95	1.89E-20	9.11E-18	-2.46	-17.31	
47	211991_s_at	HLA-DPA1	-30.06	3.96E-19	9.39E-17	-2.62	-17.26	6p21.3
48	200663_at	CD63	4.20	1.68E-17	2.01E-15	2.52	17.25	12q12-q13
49	201012_at	ANXA1	5.38	5.68E-20	2.11E-17	2.40	17.23	9q12-q21.2
50	215785_s_at	CYFIP2	-11.35	6.61E-20	2.26E-17	-2.49	-17.21	5q34

Table 2.1-2.78

2.71	AML_t(15;17) versus CML							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	212531_at	LCN2	-60.22	2.31E-32	7.69E-29	-3.79	-28.44	9q34
2	206676_at	CEACAM8	-107.43	6.58E-32	1.82E-28	-3.87	-28.38	19q13.2
3	205557_at	BPI	-34.93	1.91E-37	3.18E-33	-3.35	-27.65	20q11.23-q12
4	209771_x_at	CD24	-29.62	1.53E-36	1.28E-32	-3.28	-26.99	6q21
5	201029_s_at	CD99	6.14	1.18E-18	1.16E-16	4.19	26.60	Xp22.32
6	225386_s_at	LOC92906	-57.53	7.50E-31	1.56E-27	-3.55	-26.52	2p22.2
7	216379_x_at	KIAA1919	-29.35	5.11E-35	2.83E-31	-3.20	-26.20	6q22
8	207269_at	DEFA4	-56.93	3.35E-30	4.64E-27	-3.55	-26.03	8p23
9	211657_at	CEACAM6	-49.93	3.31E-30	4.64E-27	-3.54	-26.01	19q13.2
10	202018_s_at	LTF	-23.29	5.42E-34	2.25E-30	-3.21	-25.99	3q21-q23
11	203757_s_at	CEACAM8	-62.24	1.01E-28	1.05E-25	-3.33	-24.23	19q13.2
12	205863_at	S100A12	-37.30	5.83E-29	6.46E-26	-3.10	-23.65	1q21
13	204174_at	ALOX5AP	-22.45	1.10E-28	1.08E-25	-3.05	-23.28	13q12
14	201061_s_at	STOM	-6.06	1.29E-30	2.15E-27	-2.78	-22.52	9q34.1
15	203535_at	S100A9	-14.41	6.51E-31	1.55E-27	-2.65	-21.73	1q21
16	208650_s_at	CD24	-62.73	3.66E-27	3.08E-24	-2.87	-21.73	6q21
17	266_s_at	CD24	-50.68	4.56E-27	3.61E-24	-2.79	-21.39	6q21
18	205786_s_at	ITGAM	-13.53	3.18E-27	2.93E-24	-2.77	-21.36	16p11.2
19	231688_at		-72.42	3.70E-26	2.46E-23	-2.87	-21.11	
20	200931_s_at	VCL	-7.34	2.83E-29	3.61E-26	-2.59	-21.04	10q22.1-q23
21	223423_at	GPCR1	-13.88	1.19E-30	2.15E-27	-2.52	-20.86	3q26.2-q27
22	210244_at	CAMP	-65.83	9.06E-26	5.79E-23	-2.71	-20.40	3p21.3
23	208771_s_at	LTA4H	-6.03	3.70E-27	3.08E-24	-2.57	-20.37	12q22
24	207802_at	SGP28	-202.73	6.05E-25	2.96E-22	-2.79	-19.98	6p12.3
25	209772_s_at	CD24	-55.58	2.07E-25	1.19E-22	-2.60	-19.79	6q21
26	203467_at	PMM1	-9.53	3.22E-29	3.82E-26	-2.37	-19.65	22q13.2
27	203936_s_at	MMP9	-27.67	5.03E-25	2.53E-22	-2.59	-19.56	20q11.2-q13.1
28	201669_s_at	MARCKS	-81.40	1.88E-24	8.43E-22	-2.73	-19.47	6q22.2
29	209396_s_at	CHI3L1	-29.06	5.71E-24	2.16E-21	-2.54	-18.76	1q32.1
30	205382_s_at	DF	8.73	3.25E-14	1.02E-12	3.31	18.64	19p13.3
31	209369_at	ANXA3	-41.03	6.42E-24	2.37E-21	-2.49	-18.61	4q13-q22
32	201060_x_at	STOM	-5.63	3.46E-25	1.85E-22	-2.33	-18.49	9q34.1
33	208651_x_at	CD24	-21.00	5.26E-27	3.97E-24	-2.22	-18.30	6q21
34	217762_s_at	RAB31	-19.66	1.80E-25	1.07E-22	-2.28	-18.29	18p11.3
35	218454_at	FLJ22662	-56.46	3.33E-23	1.06E-20	-2.54	-18.19	12p13.1
36	208700_s_at	TKT	-3.61	1.57E-26	1.13E-23	-2.19	-18.07	3p14.3
37	230006_s_at	DKFZp313A2432	-7.51	1.37E-23	4.95E-21	-2.32	-17.83	11p14.2
38	204411_at	KIAA0449	-29.07	2.11E-23	7.06E-21	-2.33	-17.80	1pter-q31.3
39	226278_at	DKFZp313A2432	-6.55	2.30E-23	7.50E-21	-2.30	-17.66	11p14.2
40	226726_at	LOC129642	-9.79	1.89E-23	6.70E-21	-2.22	-17.33	2p25.2

Table 2.1-2.78

41	205033_s_at	DEFA1	-8.45	3.34E-26	2.31E-23	-2.08	-17.24	8p23.2-p23.1
42	38487_at	STAB1	42.93	4.97E-13	1.15E-11	3.68	17.15	3p21.31
43	221004_s_at	ITM2C	8.10	1.98E-13	5.06E-12	3.03	17.00	2q37
44	217764_s_at	RAB31	-12.08	3.65E-25	1.90E-22	-2.07	-16.98	18p11.3
45	227353_at	EVER2	-5.69	1.19E-25	7.34E-23	-2.05	-16.98	17q25.3
46	208438_s_at	FGR	-22.54	2.05E-24	8.97E-22	-2.09	-16.95	1p36.2-p36.1
47	205237_at	FCN1	-10.52	2.12E-23	7.06E-21	-2.10	-16.76	9q34
48	219938_s_at	PSTPIP2	-6.40	2.97E-24	1.23E-21	-2.06	-16.75	18q12
49	223663_at	FLJ37970	-10.56	3.42E-25	1.85E-22	-2.03	-16.75	11q12.3
50	211275_s_at	GYG	-3.80	2.79E-24	1.19E-21	-2.02	-16.59	3q24-q25.1
2.72	AML_t(15;17) versus normalBM							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	202018_s_at	LTF	-24.63	5.91E-09	1.27E-06	-5.08	-20.53	3q21-q23
2	205382_s_at	DF	13.86	1.72E-14	9.80E-11	4.02	19.61	19p13.3
3	201029_s_at	CD99	4.09	5.79E-17	7.53E-13	3.64	19.53	Xp22.32
4	221004_s_at	ITM2C	11.07	7.35E-14	1.91E-10	3.51	17.53	2q37
5	223280_x_at	MS4A6A	-16.24	5.22E-08	4.75E-06	-4.57	-17.38	11q12.1
6	205771_s_at	AKAP7	-10.87	1.54E-08	2.25E-06	-3.98	-16.87	6q23
7	203535_at	S100A9	-15.49	2.66E-08	3.20E-06	-3.97	-16.53	1q21
8	38487_at	STAB1	13.31	6.68E-13	1.09E-09	3.26	16.02	3p21.31
9	212953_x_at	CALR	3.79	2.26E-14	9.80E-11	2.91	15.45	19p13.3-p13.2
10	214450_at	CTSW	9.27	5.15E-14	1.67E-10	2.86	15.15	11q13.1
11	207721_x_at	HINT1	2.10	1.06E-13	2.29E-10	2.83	15.05	5q31.2
12	238022_at		13.68	2.66E-12	3.14E-09	2.91	14.53	
13	224356_x_at	MS4A6A	-16.43	4.75E-07	2.31E-05	-3.96	-14.02	11q12.1
14	217047_s_at	FAM13A1	-4.12	1.03E-09	3.28E-07	-2.83	-13.89	4q22.1
15	212531_at	LCN2	-54.83	7.71E-07	3.13E-05	-4.12	-13.56	9q34
16	205624_at	CPA3	8.50	2.87E-11	2.33E-08	2.77	13.33	3q21-q25
17	204393_s_at	ACPP	-6.05	3.22E-07	1.71E-05	-3.25	-13.10	3q21-q23
18	205349_at	GNA15	7.54	5.94E-13	1.09E-09	2.43	13.00	19p13.3
19	210192_at	ATP8A1	-4.38	2.28E-08	2.94E-06	-2.78	-12.93	4p14-p12
20	226301_at	dJ55C23.6	-6.71	8.32E-08	6.40E-06	-2.91	-12.89	6q22.3-q23.3
21	226326_at		-3.43	2.55E-12	3.14E-09	-2.39	-12.76	
22	208826_x_at	HINT1	1.78	3.47E-09	8.35E-07	2.61	12.75	5q31.2
23	225792_at		-7.31	3.87E-07	1.96E-05	-3.10	-12.64	
24	205033_s_at	DEFA1	-10.12	2.95E-07	1.60E-05	-3.02	-12.60	8p23.2-p23.1
25	231736_x_at	MGST1	3.44	1.16E-12	1.68E-09	2.31	12.42	12p12.3-p12.1
26	218262_at	FLJ22318	-3.72	2.46E-07	1.40E-05	-2.88	-12.33	5q35.3
27	224975_at	NFIA	-7.37	1.88E-07	1.18E-05	-2.81	-12.25	1p31.3-p31.2
28	239278_at		-3.94	4.24E-08	4.20E-06	-2.63	-12.23	
29	224918_x_at	MGST1	3.04	4.25E-12	4.28E-09	2.28	12.21	12p12.3-p12.1
30	202917_s_at	S100A8	-5.02	2.03E-08	2.69E-06	-2.53	-12.06	1q21
31	206488_s_at	CD36	-6.23	4.60E-09	1.07E-06	-2.41	-11.92	7q11.2

Table 2.1-2.78

32	204057_at	ICSBP1	-4.98	7.91E-07	3.19E-05	-2.94	-11.84	16q24.1
33	203645_s_at	CD163	-15.20	1.58E-06	5.14E-05	-3.23	-11.83	12p13.3
34	208612_at	GRP58	2.22	4.28E-12	4.28E-09	2.18	11.73	15q15
35	200093_s_at - HG-U133A	HINT1	1.93	8.15E-11	5.64E-08	2.21	11.62	5q31.2
36	204150_at	STAB1	17.25	4.75E-10	1.93E-07	2.45	11.48	3p21.31
37	228056_s_at	NAP1L	-30.30	2.37E-06	6.72E-05	-3.26	-11.47	19q13.33
38	212989_at	MOB	-5.21	4.76E-08	4.42E-06	-2.41	-11.43	10q
39	201596_x_at	KRT18	16.21	4.24E-10	1.80E-07	2.35	11.36	12q13
40	212509_s_at		8.35	5.37E-11	4.11E-08	2.16	11.32	
41	217225_x_at	LOC283820	2.26	1.09E-11	1.01E-08	2.10	11.27	16p13.13
42	224839_s_at	GPT2	10.99	2.68E-11	2.33E-08	2.12	11.27	16q12.1
43	226726_at	LOC129642	-6.34	1.37E-06	4.67E-05	-2.82	-11.23	2p25.2
44	202443_x_at	NOTCH2	-3.60	3.78E-10	1.75E-07	-2.15	-11.19	1p13-p11
45	202973_x_at	FAM13A1	-4.50	8.08E-08	6.25E-06	-2.38	-11.19	4q22.1
46	238365_s_at		6.97	8.25E-11	5.64E-08	2.13	11.13	
47	238949_at	FLJ31951	-8.08	5.54E-07	2.57E-05	-2.55	-11.06	5q33.3
48	225923_at		-2.35	2.04E-10	1.20E-07	-2.08	-10.99	
49	201028_s_at	CD99	6.61	3.88E-10	1.75E-07	2.17	10.95	Xp22.32
50	221030_s_at	DKFZP564B1162	-3.11	7.11E-08	5.92E-06	-2.30	-10.94	4q21.3
2.73	AML_t(8;21) versus CLL							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	224838_at	FOXP1	-5.50	3.08E-29	5.98E-25	-3.45	-25.79	3p14.1
2	203949_at	MPO	170.08	1.32E-17	2.65E-15	4.32	22.37	17q23.1
3	212827_at	IGHM	-24.48	1.51E-21	1.63E-18	-3.08	-20.47	14q32.33
4	41220_at	MSF	-2.73	4.89E-28	4.76E-24	-2.60	-20.27	17q25
5	202880_s_at	PSCD1	-6.98	2.81E-25	1.36E-21	-2.56	-19.54	17q25
6	225927_at		-3.79	1.38E-25	8.96E-22	-2.43	-18.79	
7	201811_x_at	SH3BP5	-12.98	1.33E-20	9.55E-18	-2.62	-18.25	3p24.3
8	223514_at	CARD11	-23.71	7.87E-21	6.38E-18	-2.52	-17.94	7p22
9	208091_s_at	DKFZP564K0822	-44.18	3.04E-19	1.21E-16	-2.81	-17.82	7p14.1
10	211962_s_at	ZFP36L1	-7.08	9.25E-23	2.00E-19	-2.33	-17.63	14q22-q24
11	224833_at	ETS1	-9.61	3.53E-22	5.28E-19	-2.34	-17.51	11q23.3
12	224837_at	FOXP1	-3.36	2.83E-21	2.76E-18	-2.33	-17.22	3p14.1
13	243780_at		-33.46	7.68E-19	2.62E-16	-2.66	-17.18	
14	218191_s_at	FLJ11240	-3.53	4.54E-24	1.77E-20	-2.21	-17.18	6q12
15	212590_at	RRAS2	-12.74	1.37E-18	4.16E-16	-2.60	-16.85	11p15.2
16	227979_at		-3.31	3.35E-23	9.31E-20	-2.17	-16.74	
17	208864_s_at	TXN	6.14	2.09E-16	2.58E-14	2.53	16.69	9q31
18	218029_at	FLJ13725	-4.76	1.12E-22	2.17E-19	-2.16	-16.59	16q21
19	205105_at	MAN2A1	-4.18	4.78E-22	6.64E-19	-2.16	-16.46	5q21-q22
20	208456_s_at	RRAS2	-32.68	3.36E-18	8.61E-16	-2.52	-16.37	11p15.2
21	226454_at	LOC92979	-5.08	4.03E-19	1.45E-16	-2.33	-16.36	12q13.13

Table 2.1-2.78

22	209075_s_at	NIFU	-3.12	3.87E-23	9.40E-20	-2.11	-16.36	12q24.1
23	234734_s_at	TNRC6	-3.21	3.05E-23	9.31E-20	-2.10	-16.34	16p11.2
24	212589_at	RRAS2	-28.79	5.46E-18	1.29E-15	-2.54	-16.23	11p15.2
25	216095_x_at	MTMR1	-5.27	1.77E-20	1.11E-17	-2.18	-16.21	Xq28
26	224579_at		-6.33	7.92E-20	4.05E-17	-2.22	-16.20	
27	204118_at	CD48	-5.82	1.09E-20	8.18E-18	-2.15	-16.12	1q21.3-q22
28	203948_s_at	MPO	300.08	2.40E-14	1.25E-12	3.15	16.06	17q23.1
29	212313_at	MGC29816	-7.09	2.74E-19	1.11E-16	-2.23	-16.03	8p21.2
30	219869_s_at	BIGM103	6.25	5.31E-15	3.60E-13	2.62	16.01	4q22-q24
31	221718_s_at	AKAP13	-3.37	1.39E-22	2.45E-19	-2.04	-15.88	15q24-q25
32	226538_at		-5.38	1.12E-19	4.82E-17	-2.14	-15.75	
33	218237_s_at	SLC38A1	-5.76	9.56E-20	4.43E-17	-2.12	-15.65	12q12
34	39582_at		-5.14	5.89E-21	5.20E-18	-2.06	-15.65	
35	208657_s_at	MSF	-5.47	1.38E-19	5.83E-17	-2.12	-15.63	17q25
36	212386_at		-20.38	1.59E-17	3.10E-15	-2.42	-15.62	
37	213151_s_at	CDC10	-2.15	2.85E-22	4.62E-19	-2.00	-15.59	7p14.3-p14.1
38	204951_at	ARHH	-6.59	3.36E-19	1.26E-16	-2.14	-15.56	4p13
39	234140_s_at	STIM2	-6.45	5.25E-18	1.28E-15	-2.24	-15.45	4p15.2
40	225246_at	STIM2	-7.51	2.32E-18	6.09E-16	-2.17	-15.40	4p15.2
41	211084_x_at	PRKCN	-8.56	1.08E-19	4.80E-17	-2.06	-15.32	2p21
42	207000_s_at	PPP3CC	-5.62	1.81E-18	5.02E-16	-2.13	-15.25	8p21.2
43	211709_s_at	SCGF	39.67	7.60E-14	3.21E-12	2.92	15.22	19q13.3
44	228390_at		-32.75	4.33E-17	7.20E-15	-2.40	-15.22	
45	44790_s_at	C13orf18	-46.55	6.00E-17	9.41E-15	-2.44	-15.12	13q14.11
46	227261_at	KLF12	-8.19	2.09E-18	5.56E-16	-2.10	-15.10	13q22
47	214615_at	P2RY10	-9.48	3.73E-18	9.42E-16	-2.12	-15.08	Xq21.1
48	217941_s_at	ERBB2IP	-2.81	7.24E-22	9.39E-19	-1.93	-15.06	5q12.2
49	218236_s_at	PRKCN	-12.62	1.05E-17	2.17E-15	-2.16	-15.04	2p21
50	223287_s_at	FOXP1	-4.70	3.02E-18	7.82E-16	-2.10	-15.04	3p14.1
2.74	AML_t(8;21) versus CML							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	225386_s_at	LOC92906	-12.32	3.21E-32	6.78E-28	-2.43	-20.92	2p22.2
2	207802_at	SGP28	-239.28	5.80E-25	2.04E-21	-2.78	-19.99	6p12.3
3	201425_at	ALDH2	-12.66	2.95E-30	3.11E-26	-2.33	-19.91	12q24.2
4	203936_s_at	MMP9	-11.57	2.49E-25	1.05E-21	-2.10	-17.48	20q11.2-q13.1
5	210244_at	CAMP	-10.52	8.63E-26	6.07E-22	-1.98	-16.83	3p21.3
6	202391_at	BASP1	-9.03	1.64E-25	8.66E-22	-1.97	-16.72	5p15.1-p14
7	218454_at	FLJ22662	-12.67	2.58E-23	5.45E-20	-1.92	-15.96	12p13.1
8	205653_at	CTSG	-6.90	7.36E-25	2.22E-21	-1.85	-15.83	14q11.2
9	208091_s_at	DKFZP564K0822	-6.86	3.77E-24	9.95E-21	-1.85	-15.70	7p14.1
10	201700_at	CCND3	-3.45	8.94E-24	2.09E-20	-1.77	-15.16	6p21
11	200985_s_at	CD59	-6.92	7.39E-23	1.30E-19	-1.76	-14.92	11p13

Table 2.1-2.78

12	208438_s_at	FGR	-5.53	2.74E-21	3.21E-18	-1.75	-14.54	1p36.2-p36.1
13	224595_at	CDW92	-6.63	6.18E-23	1.18E-19	-1.68	-14.44	9q31.2
14	224596_at	CDW92	-6.23	1.70E-22	2.77E-19	-1.67	-14.35	9q31.2
15	230006_s_at	DKFZp313A2432	-4.72	1.99E-22	2.99E-19	-1.67	-14.32	11p14.2
16	220558_x_at	PHEMX	-2.68	3.10E-22	4.35E-19	-1.66	-14.21	11p15.5
17	213908_at		-5.66	2.96E-21	3.21E-18	-1.68	-14.16	
18	212531_at	LCN2	-4.85	1.90E-19	1.25E-16	-1.72	-14.15	9q34
19	202119_s_at	CPNE3	-6.40	2.54E-21	3.21E-18	-1.61	-13.72	8q21.13
20	200983_x_at	CD59	-6.13	3.03E-21	3.21E-18	-1.60	-13.65	11p13
21	233467_s_at	PHEMX	-2.93	3.05E-21	3.21E-18	-1.56	-13.40	11p15.5
22	230285_at	DKFZp313A2432	-4.48	9.77E-21	8.96E-18	-1.57	-13.39	11p14.2
23	205237_at	FCN1	-6.12	3.38E-21	3.39E-18	-1.56	-13.38	9q34
24	227019_at		-3.17	7.45E-21	7.14E-18	-1.56	-13.34	
25	221581_s_at	WBSCR5	-6.46	3.65E-19	2.14E-16	-1.61	-13.22	7q11.23
26	209395_at	CHI3L1	-13.40	2.63E-19	1.63E-16	-1.58	-13.11	1q32.1
27	219010_at	FLJ10901	-3.67	1.81E-20	1.53E-17	-1.53	-13.11	1q31.3
28	210254_at	MS4A3	-2.64	1.68E-18	7.70E-16	-1.57	-13.05	11q12
29	226278_at	DKFZp313A2432	-3.95	1.79E-20	1.53E-17	-1.50	-12.94	11p14.2
30	217963_s_at	NGFRAP1	-19.46	1.63E-17	5.14E-15	-1.66	-12.81	Xq22.1
31	235044_at	CYYR1	-7.78	1.63E-18	7.66E-16	-1.56	-12.80	21q21.2
32	200984_s_at	CD59	-4.56	8.10E-19	4.40E-16	-1.54	-12.80	11p13
33	211178_s_at	PSTPIP1	-3.95	4.37E-20	3.54E-17	-1.49	-12.79	15q24-q25.1
34	213353_at	ABCA5	-3.37	5.16E-20	4.03E-17	-1.49	-12.75	17q24.3
35	210146_x_at	LILRB2	-7.53	1.73E-18	7.76E-16	-1.53	-12.67	19q13.4
36	206515_at	CYP4F3	-12.82	6.16E-18	2.17E-15	-1.57	-12.67	19p13.2
37	209396_s_at	CHI3L1	-7.09	1.23E-19	8.91E-17	-1.48	-12.64	1q32.1
38	236979_at		-3.19	1.41E-19	9.59E-17	-1.48	-12.64	
39	205627_at	CDA	-9.39	1.94E-18	8.53E-16	-1.52	-12.58	1p36.2-p35
40	207814_at	DEFA6	-5.20	1.39E-19	9.59E-17	-1.46	-12.54	8pter-p21
41	229373_at		-2.95	1.12E-19	8.45E-17	-1.45	-12.48	
42	227236_at	TSPAN-2	-10.33	2.22E-18	9.57E-16	-1.49	-12.46	1p12
43	212463_at		-4.90	8.39E-19	4.43E-16	-1.46	-12.36	
44	219014_at	PLAC8	-2.98	2.34E-19	1.49E-16	-1.44	-12.34	4q21.3
45	225009_at	CKLFSF4	-3.85	3.56E-19	2.14E-16	-1.43	-12.26	16q21
46	212828_at	SYNJ2	-3.60	1.42E-18	6.80E-16	-1.44	-12.22	6q25.3
47	208771_s_at	LTA4H	-2.59	7.30E-19	4.16E-16	-1.41	-12.08	12q22
48	206440_at	LIN7A	-5.17	1.19E-18	5.98E-16	-1.41	-12.07	12q21
49	202006_at	PTPN12	-3.03	8.14E-19	4.40E-16	-1.40	-12.04	7q11.23
50	203922_s_at	CYBB	-7.48	6.11E-17	1.59E-14	-1.50	-12.04	Xp21.1
2.75	AML_t(8;21) versus normalBM							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	227041_at		-3.68	4.06E-13	2.02E-09	-2.67	-14.96	
2	201425_at	ALDH2	-11.12	8.11E-09	2.88E-06	-3.09	-14.81	12q24.2

Table 2.1-2.78

3	206488_s_at	CD36	-6.91	7.14E-08	1.17E-05	-3.00	-13.60	7q11.2
4	212828_at	SYNJ2	-3.49	5.73E-09	2.31E-06	-2.59	-13.09	6q25.3
5	227388_at		-4.89	1.16E-07	1.65E-05	-2.84	-12.89	
6	209122_at	ADFP	4.63	5.55E-14	8.28E-10	2.19	12.73	9p21.3
7	208690_s_at	PDLIM1	5.84	2.48E-12	9.26E-09	2.18	12.12	10q22-q26.3
8	225923_at		-2.49	6.95E-11	1.29E-07	-2.15	-11.96	
9	209732_at	CLECSF2	3.71	3.76E-13	2.02E-09	2.03	11.81	12p13-p12
10	225792_at		-5.22	5.78E-07	4.74E-05	-2.73	-11.77	
11	224975_at	NFIA	-5.91	1.88E-07	2.16E-05	-2.48	-11.62	1p31.3-p31.2
12	228056_s_at	NAP1L	-32.93	2.60E-06	1.16E-04	-3.43	-11.56	19q13.33
13	208146_s_at	CPVL	-17.78	2.12E-06	1.03E-04	-3.14	-11.51	7p15-p14
14	204767_s_at	FEN1	-2.47	9.17E-10	7.19E-07	-2.06	-11.25	11q12
15	226301_at	dJ55C23.6	-4.23	6.80E-08	1.15E-05	-2.20	-10.98	6q22.3-q23.3
16	218262_at	FLJ22318	-3.19	7.77E-08	1.22E-05	-2.14	-10.76	5q35.3
17	213908_at		-3.85	5.90E-08	1.04E-05	-2.12	-10.72	
18	240572_s_at		-4.51	6.69E-07	5.23E-05	-2.26	-10.45	
19	208091_s_at	DKFZP564K0822	-7.91	2.35E-06	1.08E-04	-2.49	-10.38	7p14.1
20	201506_at	TGFBI	-15.58	4.90E-06	1.70E-04	-2.83	-10.36	5q31
21	217815_at	SUPT16H	-1.91	2.54E-11	6.32E-08	-1.79	-10.35	14q11.1
22	226806_s_at		-7.79	3.36E-06	1.37E-04	-2.59	-10.32	
23	212419_at	FLJ90798	-3.25	1.44E-08	3.91E-06	-1.92	-10.22	10q22.3
24	224976_at	NFIA	-4.62	1.64E-06	8.85E-05	-2.30	-10.16	1p31.3-p31.2
25	238756_at		-4.87	2.98E-06	1.26E-04	-2.42	-10.09	
26	207243_s_at	CALM2	-1.89	1.39E-10	2.30E-07	-1.76	-10.08	2p21
27	217047_s_at	FAM13A1	-2.45	6.67E-09	2.62E-06	-1.84	-10.03	4q22.1
28	209545_s_at	RIPK2	2.56	2.29E-11	6.32E-08	1.72	10.01	8q21
29	228827_at		67.21	4.96E-10	5.28E-07	1.98	9.99	
30	239278_at		-3.07	1.75E-08	4.29E-06	-1.87	-9.98	
31	223044_at	SLC11A3	-6.37	1.29E-06	7.57E-05	-2.18	-9.95	2q32
32	200833_s_at	RAP1B	-2.05	3.87E-09	1.98E-06	-1.80	-9.90	12q14
33	226326_at		-2.61	5.16E-11	1.10E-07	-1.70	-9.89	
34	202443_x_at	NOTCH2	-2.59	5.05E-09	2.09E-06	-1.78	-9.82	1p13-p11
35	201015_s_at	JUP	19.68	5.54E-10	5.50E-07	1.83	9.78	17q21
36	213624_at	ASM3A	-5.01	3.32E-06	1.36E-04	-2.30	-9.77	6
37	236297_at		-3.05	9.94E-07	6.42E-05	-2.05	-9.68	
38	208908_s_at	CAST	-3.55	1.54E-07	1.93E-05	-1.89	-9.66	5q15-q21
39	223515_s_at	COQ3	-2.13	1.17E-09	8.28E-07	-1.69	-9.54	6q16.3
40	236305_at	LOC317671	-4.66	3.60E-06	1.45E-04	-2.18	-9.47	
41	202018_s_at	LTF	-3.03	2.95E-10	3.66E-07	-1.64	-9.45	3q21-q23
42	223256_at	FLJ20333	-2.34	7.40E-08	1.19E-05	-1.79	-9.45	14q12
43	202561_at	TNKS	-2.21	1.26E-09	8.56E-07	-1.66	-9.40	8p23.1
44	206940_s_at	POU4F1	29.25	1.70E-09	1.08E-06	1.81	9.35	13q21.1-q22
45	204057_at	ICSBP1	-2.97	1.33E-06	7.73E-05	-1.96	-9.30	16q24.1
46	226460_at	KIAA1450	-2.86	1.73E-07	2.06E-05	-1.79	-9.27	4q32.1
47	201988_s_at	CREBL2	-1.93	9.37E-09	3.12E-06	-1.67	-9.23	12p13
48	217846_at	QARS	1.62	6.59E-10	5.78E-07	1.61	9.22	3p21.3-p21.1

Table 2.1-2.78

49	209054_s_at	WHSC1	-2.25	6.35E-08	1.10E-05	-1.72	-9.17	4p16.3
50	201029_s_at	CD99	3.20	2.46E-10	3.39E-07	1.58	9.17	Xp22.32
2.76	CLL versus CML							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	206871_at	ELA2	-240.77	1.06E-35	1.75E-32	-4.68	-34.45	19p13.3
2	212268_at	SERPINB1	-9.53	2.70E-42	3.99E-38	-3.87	-33.91	6p25
3	210254_at	MS4A3	-56.91	2.43E-35	3.59E-32	-4.01	-31.87	11q12
4	205557_at	BPI	-83.16	4.03E-34	3.73E-31	-4.04	-31.07	20q11.23-q12
5	203949_at	MPO	-162.81	4.55E-33	3.21E-30	-4.19	-30.37	17q23.1
6	200654_at	P4HB	-5.02	1.63E-40	1.20E-36	-3.42	-30.32	17q25
7	213572_s_at	SERPINB1	-6.93	3.67E-38	1.81E-34	-3.42	-29.68	6p25
8	202503_s_at	KIAA0101	-37.72	6.41E-32	3.06E-29	-3.84	-28.46	15q22.1
9	224838_at	FOXP1	6.62	1.88E-27	3.30E-25	3.84	28.37	3p14.1
10	206676_at	CEACAM8	-72.60	2.86E-32	1.51E-29	-3.60	-28.04	19q13.2
11	206111_at	RNASE2	-45.25	3.07E-32	1.57E-29	-3.59	-27.98	14q24-q31
12	209619_at	CD74	5.87	4.99E-36	1.21E-32	3.16	27.73	5q32
13	212531_at	LCN2	-45.41	1.94E-33	1.43E-30	-3.37	-27.72	9q34
14	204670_x_at	HLA-DRB5	6.98	4.97E-31	1.99E-28	3.28	27.25	6p21.3
15	211657_at	CEACAM6	-50.24	2.89E-30	8.53E-28	-3.45	-25.99	19q13.2
16	207269_at	DEFA4	-48.94	9.09E-31	3.05E-28	-3.24	-25.65	8p23
17	208306_x_at	HLA-DRB4	7.48	3.61E-29	8.75E-27	3.13	25.65	6p21.3
18	201061_s_at	STOM	-14.74	5.26E-33	3.53E-30	-3.00	-25.47	9q34.1
19	214575_s_at	AZU1	-236.51	2.96E-29	7.53E-27	-3.53	-25.09	19p13.3
20	202018_s_at	LTF	-22.71	1.05E-35	1.75E-32	-2.82	-25.02	3q21-q23
21	202252_at	RAB13	-11.58	6.31E-31	2.39E-28	-3.06	-24.97	1q21.2
22	208864_s_at	TXN	-7.21	2.75E-34	2.71E-31	-2.85	-24.92	9q31
23	208700_s_at	TKT	-8.05	4.28E-37	1.26E-33	-2.76	-24.87	3p14.3
24	202589_at	TYMS	-40.46	6.71E-29	1.50E-26	-3.32	-24.47	18p11.32
25	203675_at	NUCB2	-40.18	4.55E-29	1.05E-26	-3.24	-24.45	11p15.1-p14
26	203757_s_at	CEACAM6	-93.21	8.45E-29	1.81E-26	-3.32	-24.37	19q13.2
27	211275_s_at	GYG	-6.92	1.10E-31	4.95E-29	-2.88	-24.33	3q24-q25.1
28	201554_x_at	GYG	-10.43	5.72E-31	2.23E-28	-2.88	-24.03	3q24-q25.1
29	205653_at	CTSG	-125.96	2.60E-28	5.19E-26	-3.34	-23.88	14q11.2
30	201432_at	CAT	-5.01	1.40E-37	5.19E-34	-2.60	-23.77	11p13
31	208308_s_at	GPI	-5.19	6.27E-32	3.06E-29	-2.76	-23.69	19q13.1
32	203948_s_at	MPO	-273.73	4.50E-28	8.76E-26	-3.30	-23.59	17q23.1
33	202487_s_at	H2AV	-4.05	1.26E-32	7.46E-30	-2.70	-23.56	7p13
34	203021_at	SLPI	-24.64	2.43E-28	4.93E-26	-3.08	-23.46	20q12
35	202441_at	KEO4	-10.82	3.95E-29	9.42E-27	-2.93	-23.43	10q21-q22
36	210140_at	CST7	-11.66	1.41E-30	4.50E-28	-2.76	-23.28	20p11.21

Table 2.1-2.78

37	226905_at		-11.36	1.49E-33	1.16E-30	-2.60	-23.08	
38	208699_x_at	TKT	-10.41	8.12E-34	7.06E-31	-2.58	-22.99	3p14.3
39	41220_at	MSF	2.59	1.85E-31	7.97E-29	2.59	22.78	17q25
40	210613_s_at	SYNGR1	-22.29	6.96E-29	1.54E-26	-2.77	-22.63	22q13.1
41	225927_at		4.67	8.70E-25	8.46E-23	2.92	22.56	
42	201012_at	ANXA1	-7.02	5.73E-36	1.21E-32	-2.43	-22.30	9q12-q21.2
43	205513_at	TCN1	-40.38	3.43E-27	5.58E-25	-2.94	-22.21	11q11-q12
44	204351_at	S100P	-18.25	1.49E-30	4.60E-28	-2.55	-22.06	4p16
45	209312_x_at	HLA-DRB1	6.36	6.49E-27	1.01E-24	2.65	22.01	6p21.3
46	201663_s_at	SMC4L1	-4.55	7.78E-31	2.74E-28	-2.50	-21.78	3q26.1
47	219076_s_at	PXMP2	-6.65	3.14E-30	8.98E-28	-2.51	-21.71	12q24.33
48	201060_x_at	STOM	-17.56	3.08E-27	5.11E-25	-2.76	-21.71	9q34.1
49	221952_x_at	KIAA1393	-2.49	1.13E-33	9.24E-31	-2.38	-21.56	14q23.1
50	AFFX-HUMGAPDH/M33197_M_at - HG-U133A	GAPD	-3.70	6.01E-35	8.08E-32	-2.35	-21.51	12p13
2.77	CLL versus normalBM							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	202018_s_at	LTF	-24.02	2.31E-09	6.07E-08	-4.21	-20.09	3q21-q23
2	210613_s_at	SYNGR1	-23.75	2.96E-08	5.29E-07	-4.74	-18.95	22q13.1
3	204285_s_at	PMAIP1	11.02	2.58E-21	3.52E-17	2.84	18.74	18q21.31
4	224838_at	FOXP1	4.00	2.81E-17	3.20E-14	2.91	18.66	3p14.1
5	218424_s_at	TSAP6	-5.59	7.11E-10	2.26E-08	-3.39	-17.84	2q14.1
6	218662_s_at	HCAP-G	-12.98	5.93E-08	9.56E-07	-4.53	-17.71	4p16-p15
7	218257_s_at	UGCGL1	-2.50	6.15E-14	1.17E-11	-2.67	-16.60	2q14.3
8	204215_at	MGC4175	3.99	7.21E-20	4.92E-16	2.41	16.16	7q21.1-q21.2
9	217478_s_at	HLA-DMA	3.53	1.45E-19	6.59E-16	2.40	16.06	6p21.3
10	208456_s_at	RRAS2	19.73	4.25E-18	8.28E-15	2.48	15.89	11p15.2
11	201200_at	CREG	-4.15	3.27E-12	2.70E-10	-2.60	-15.70	1q24
12	204767_s_at	FEN1	-3.38	6.31E-09	1.44E-07	-3.04	-15.60	11q12
13	243780_at		9.48	3.09E-18	8.28E-15	2.34	15.36	
14	201858_s_at	PRG1	-3.95	2.54E-10	9.80E-09	-2.71	-15.33	10q22.1
15	AFFX-HUMGAPDH/M33197_3_at - HG-U133B	GAPD	-2.16	2.35E-13	3.11E-11	-2.44	-15.22	12p13
16	212589_at	RRAS2	15.19	3.80E-18	8.28E-15	2.28	15.10	11p15.2
17	204286_s_at	PMAIP1	18.90	4.77E-17	4.65E-14	2.36	14.94	18q21.31
18	212590_at	RRAS2	6.88	3.72E-18	8.28E-15	2.21	14.74	11p15.2
19	208091_s_at	DKFZP564K0822	5.58	2.32E-17	2.88E-14	2.21	14.50	7p14.1
20	209306_s_at	SWAP70	7.91	1.36E-17	2.06E-14	2.18	14.43	11p15
21	205051_s_at	KIT	-8.06	1.02E-07	1.50E-06	-3.17	-14.42	4q11-q12
22	229872_s_at	FLJ23790	3.69	5.60E-18	9.55E-15	2.14	14.37	8q24.13
23	202165_at	PPP1R2	3.38	1.51E-15	5.07E-13	2.17	14.22	3q29

Table 2.1-2.78

24	226043_at	AGS3	-2.57	2.15E-11	1.31E-09	-2.36	-14.21	9q34.3
25	225927_at		2.75	1.23E-14	3.11E-12	2.18	14.12	
26	223391_at	SGPP1	6.71	9.88E-17	8.42E-14	2.15	14.05	14q23.1
27	207000_s_at	PPP3CC	5.68	1.53E-17	2.08E-14	2.09	14.01	8p21.2
28	239287_at		20.36	5.19E-16	2.72E-13	2.24	13.97	
29	44790_s_at	C13orf18	11.58	3.09E-16	1.76E-13	2.19	13.97	13q14.11
30	212386_at		7.60	1.28E-16	1.03E-13	2.14	13.96	
31	212827_at	IGHM	4.93	2.29E-16	1.42E-13	2.11	13.96	14q32.33
32	235733_at		-2.97	4.50E-11	2.46E-09	-2.32	-13.89	
33	228390_at		9.09	3.63E-16	1.98E-13	2.15	13.79	
34	206845_s_at	RNF40	-2.60	2.19E-08	4.13E-07	-2.67	-13.76	16p11.2-p11.1
35	227388_at		-5.25	3.46E-07	4.17E-06	-3.29	-13.69	
36	203194_s_at	NUP98	-2.20	1.46E-13	2.17E-11	-2.14	-13.68	11p15.5
37	202503_s_at	KIAA0101	-32.35	7.79E-07	8.02E-06	-4.21	-13.64	15q22.1
38	209374_s_at	IGHM	5.52	4.61E-17	4.65E-14	2.02	13.54	14q32.33
39	224975_at	NFIA	-11.22	4.28E-07	4.91E-06	-3.31	-13.52	1p31.3-p31.2
40	225230_at		2.90	1.59E-16	1.14E-13	2.03	13.46	
41	212531_at	LCN2	-41.35	6.83E-07	7.21E-06	-3.59	-13.40	9q34
42	201432_at	CAT	-4.57	7.50E-08	1.17E-06	-2.73	-13.39	11p13
43	223253_at	UCC1	-5.10	4.82E-07	5.41E-06	-3.28	-13.35	7p14.1
44	223287_s_at	FOXP1	4.29	9.34E-17	8.42E-14	1.99	13.34	3p14.1
45	205909_at	POLE2	-5.29	3.54E-07	4.22E-06	-3.10	-13.31	14q21-q22
46	219471_at	C13orf18	7.78	1.21E-15	4.33E-13	2.05	13.23	13q14.11
47	213113_s_at	EEG1	-3.71	2.87E-07	3.55E-06	-2.97	-13.20	11q11
48	204674_at	LRMP	4.68	8.59E-16	3.55E-13	2.02	13.17	12p12.1
49	203057_s_at	PRDM2	4.43	1.36E-16	1.03E-13	1.96	13.15	1p36
50	228249_at	LOC119710	-7.89	5.06E-07	5.64E-06	-3.18	-13.14	11p12
2.78	CML versus normalBM							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	218184_at	TUSP	-3.12	8.20E-11	3.85E-08	-2.62	-16.24	6q25-q26
2	203725_at	GADD45A	3.60	6.10E-20	1.15E-15	1.91	14.45	1p31.2-p31.1
3	204805_s_at	TGM2	4.50	1.70E-19	1.60E-15	1.84	14.00	20q12
4	206206_at	LY64	-3.39	2.54E-09	4.54E-07	-2.22	-13.46	5q12
5	223280_x_at	MS4A6A	-2.98	2.05E-07	1.25E-05	-2.16	-11.63	11q12.1
6	209357_at	CITED2	3.51	3.63E-16	1.54E-12	1.53	11.59	6q23.3
7	207980_s_at	CITED2	4.26	4.09E-16	1.54E-12	1.53	11.57	6q23.3
8	225829_at	LOC118987	3.29	4.01E-16	1.54E-12	1.52	11.53	10q26.12
9	202561_at	TNKS	-2.17	7.65E-09	9.98E-07	-1.77	-11.16	8p23.1
10	203073_at	COG2	-1.96	4.84E-08	4.03E-06	-1.86	-11.08	1q42.13
11	228056_s_at	NAP1L	-12.92	2.64E-06	9.29E-05	-2.53	-10.83	19q13.33
12	226326_at		-2.11	1.79E-10	6.18E-08	-1.53	-10.61	
13	201917_s_at	FLJ10618	2.94	1.48E-12	2.32E-09	1.38	10.15	3q23
14	218251_at	STRAIT11499	3.28	4.28E-13	8.04E-10	1.36	10.15	Xp11.4

Table 2.1-2.78

15	201186_at	LRPAP1	2.84	2.37E-13	6.36E-10	1.34	10.05	4p16.3
16	214109_at	LRBA	-1.61	5.25E-13	8.97E-10	-1.34	-10.02	4q31.22-q31.23
17	225923_at		-1.83	2.03E-08	2.01E-06	-1.56	-10.01	
18	208909_at	UQCRFS1	1.48	2.97E-12	3.28E-09	1.35	9.93	19q12-q13.1
19	203645_s_at	CD163	-5.60	1.47E-08	5.97E-05	-1.90	-9.90	12p13.3
20	202070_s_at	IDH3A	-2.11	1.14E-07	7.92E-06	-1.62	-9.89	15q25.1-q25.2
21	204057_at	ICSBP1	-3.19	1.50E-06	6.04E-05	-1.89	-9.87	16q24.1
22	205633_s_at	ALAS1	2.74	2.91E-13	6.83E-10	1.31	9.85	3p21.1
23	206200_s_at	ANXA11	2.17	1.74E-13	5.46E-10	1.30	9.82	10q23
24	224356_x_at	MS4A6A	-3.10	3.02E-06	1.03E-04	-2.02	-9.78	11q12.1
25	208499_s_at	DNAJC3	3.52	3.14E-11	2.27E-08	1.31	9.53	13q32
26	225830_at	LOC118987	2.91	4.10E-13	8.04E-10	1.24	9.41	10q26.12
27	209893_s_at	FUT4	3.16	3.90E-11	2.72E-08	1.28	9.36	11q21
28	237209_s_at	NFRKB	2.34	6.73E-12	6.03E-09	1.25	9.28	11q24-q25
29	227388_at		-2.40	1.35E-06	5.65E-05	-1.66	-9.23	
30	226301_at	dJ55C23.6	-2.79	4.01E-07	2.07E-05	-1.53	-9.16	6q22.3-q23.3
31	217047_s_at	FAM13A1	-2.01	1.30E-07	8.65E-06	-1.45	-9.12	4q22.1
32	214882_s_at	SFRS2	1.67	1.35E-10	5.19E-08	1.25	9.10	17q25.3
33	239105_at		2.57	2.77E-12	3.27E-09	1.20	9.09	
34	226713_at	C3orf6	-2.96	3.18E-06	1.07E-04	-1.74	-9.08	3q29
35	224572_s_at		2.50	1.54E-10	5.66E-08	1.25	9.04	
36	212420_at	ELF1	2.70	3.30E-12	3.44E-09	1.19	9.03	13q13
37	218472_s_at	PELO	2.94	2.05E-12	2.97E-09	1.18	8.97	5q11.2
38	204011_at	SPRY2	4.43	2.30E-12	3.09E-09	1.18	8.96	13q22.1
39	214108_at	MAX	4.28	2.78E-12	3.27E-09	1.18	8.94	14q23
40	208864_s_at	TXN	1.93	4.83E-08	4.03E-06	1.36	8.93	9q31
41	213503_x_at	ANXA2	-3.38	1.02E-05	2.74E-04	-1.98	-8.90	15q21-q22
42	208683_at	CAPN2	-3.43	1.02E-05	2.73E-04	-1.95	-8.86	1q41-q42
43	204039_at	CEBPA	2.56	4.80E-10	1.30E-07	1.23	8.85	19q13.1
44	216652_s_at		1.81	6.64E-12	6.03E-09	1.16	8.82	
45	226835_s_at		1.73	1.88E-10	6.18E-08	1.21	8.81	
46	218036_x_at	CGI-07	2.35	6.95E-11	3.62E-08	1.18	8.76	3q26.1
47	205681_at	BCL2A1	3.41	7.37E-12	6.30E-09	1.16	8.76	15q24.3
48	232098_at		-2.74	1.74E-07	1.09E-05	-1.37	-8.74	
49	201918_at	FLJ10618	2.30	5.58E-11	3.35E-08	1.17	8.72	3q23
50	217815_at	SUPT16H	-1.62	2.77E-10	8.02E-08	-1.20	-8.72	14q11.1